

493 CCCCTGGGTTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATCGCCTGGTCAAGGCCT 555

504 CCCCTGTGTGGAGGTACAACCTGGCTCCTCGGTGACTTAGGATGCCCTGGTCAAGGTT 563

553 ACTTCCCCTGAGTGAAGTGAAGTGTGACTTGGAACCTGGATCCCTGTCAGAGCTGAGCTGCCA 612

564 ATTTCCTGAGCCAGTGAATTGACTTGAACTGGAACTCTGGATCCCTGTCCAGTGGTGACA 623

613 CTTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGAAGTGTCCCT 672

624 CTTTCCCAGCTCTCCTGCAGTCTGGCTCTTACACCTCTCAGAGCTCAGTGAAGTGAAGCT 683

673 CCAGCACCTGGCCAAAGTCAGACCGTCAACCTGCAGCGTTGCTCACCAGCCAGCAGCACCA 732

684 CGAACACCTGGCCAGCCAGCACCATCACTTGCATGTGGCCACCGCCGGAAGCAGCACCA 743

733 CGGTGGACAAAAAATTGAGCCAGCGGGGCCATTCAAACATCAACCCCTGCTCCTCAT 792

744 AAGTGGACAAGAANAATTGAGCCAGAGTGGCCAT---AACACGAAGCCCTGCTCCTCCAC 800

793 GGAAGGAGTGTCAAAATGCCAGCTCTTAACCTCGAGGGTGGACATCCGCTCTTCATCT 852

801 TCAAAGAGTGTCCCCATGGCAGCTCCAGACCTCTTGGGTGGACCATCOGCTCTTCATCT 860

853 TCCCTCCAATAATCAAGGATGTACTCATGATCTCCCTGACACCCAGGTCAAGTGTGTGG 912

861 TCCCTCCAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATGGTTCATGTGTGG 920

913 TGGTGGATGTGAGGAGGATGCCAGAGCTCCAGATCAGCTGTTGTGAACAACTGG 972

921 TGGTGGATGTGAGGAGGATGCCAGAGCTCCAGATCAGCTGTTGTGAACAACTGG 980

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981 AAGTACACACAGCTCAGACAAAACCCATAGAGAGGATTACACAGTACTATCCGGGTGG 1040

1033 TCAGCACCTTCCCATCCAGCACCGAGCTGGATGAGTGGCAAGGAGTCAAATGCAAGG 1092

1041 TCAGTGGCTTCCCATCCAGCACCGAGCTGGATGAGTGGCAAGGAGTCAAATGCAAGG 1100

1093 TCAACAAACAAGACCTCCCATCCCATCCAGACCGAGAACCATCTCAAAATTAAGGGCTAG 1152

1101 TCAACAAACAGAGCTTCCCATCCCATCCAGAAACCATCTCAAAACCCAGAGGGCCAG 1160

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1341 CTTACTTTCATGACAGCAAGCTCAGAGTACAAAAGAGACACTTGGGAAGAGGAGTCTTT 1400

1393 TCTCATGCAACGTGACACAGAGGCTGTGAAAATTAATCACTGTGAAGAGAACCATCTCCC 1452

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1513 CCCATATCCATGCATCCCTTGTATTAATTAAGCATCCAGCAAGCCCTGGTACCATG 1568

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RESULT 2	ACCESSION	REFERENCE	FEATURES	BASE COUNT	Query Match
BG0711858/c	VERSION	AUTHORS	source	ORIGIN	Best Loca
LOCUS	KEYWORDS	TITLE	JOURNAL		Matches
DEFINITION	SOURCE	COMMENT			
	ORGANISM				
					70
					80

BG071858 842 bp mRNA linear EST 26-JAN-2001
 H3103H12-3 N1A Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 H3103H12 3', mRNA sequence.
 BG071858
 BG071858.1 GI:12554427
 EST
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 842)
 Kargul,D.G., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
 ,T.S., Carter,M.G. and Ko,M,S.H.
 Verification and initial annotation of N1A mouse 15K cDNA clone set
 Unpublished (2001)
 Other_ESTs: H3103H12-5
 Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3103 row: H column: 12
 seq primer: -21M13 Forward
 High quality sequence stop: 842
 POLYA=yes

FEATURES	source
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/lab_host="DH10B"	
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162 a	192 c 237 q
	251 t

BASE COUNT

ORIGIN

Query Match	52.3%;	Score 830.8;	DB 12;	Length 842;
Best Local Similarity	99.2%;	Pred. No. 4.4e-162;		

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Db	842	GCTCACCACCCAGCAGCACCGGTGGACAAAACCTTGAGCCCCAGGGGCCCATTTCA	783
QY	771	ACAAATCAACCCCTGTCTCTCAATCAAGAGAGTGTCAAAATGCCAGCTCTTAACTCGAG	830

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||||| 831 GTGGGACCACTCCCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGTCTCCCTG 890
||||| 722 GTGGGACCACTCCCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGTCTCCCTG 663
||||| 891 ACACCAAGGTACAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 950
||||| 662 ACACCAAGGTACAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 603
||||| 951 AGCTGTTTGTGAACACAGTGGAGTACACACAGCTCAGACACAAACCCATAGAGAGAT 1010
||||| 602 AGCTGTTTGTGAACACAGTGGAGTACACACAGCTCAGACACAAACCCATAGAGAGAT 543
||||| 1011 TACAACAGTACTATCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1070
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||||| 1071 GCGAAGGATTCAAATCAAGGTCAACAAAGACCTCCCATCCAGCACCCATCGAGAGACC 1130
||||| 482 GCGAAGGATTCAAATCAAGGTCAACAAAGACCTCCCATCCAGCACCCATCGAGAGACC 423
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||||| 1191 GAGCAGTGTGTCAGGAAAGATGTGAGTCTCACTTCCCTGGTGGTGGTGGTGGTGGTGGT 1250
||||| 362 GAGCAGTGTGTCAGGAAAGATGTGAGTCTCACTTGGCTGGTGGTGGTGGTGGTGGTGGT 303
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||||| 1311 CCAGTCTGGAGTGTGAGGTTCTTACTTCTATATATACAGAGCTCAATATGAAACAAAGC 1370
||||| 242 CCAGTCTGGAGTGTGAGGTTCTTACTTCTATATACAGAGCTCGATATAAAACAAAGC 183
||||| 1371 AAGTGGGAGAAACAGATTCCTTCTCATCAAGTGGAGACAGAGGCTCTGAAAATATAC 1430
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||||| 122 TACCTGAAGAGACCATCTCCGGTCTCCGGTAAATGAGCTCAGACCCCAAGAGTCT 63
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||||| 2 GC 1

BE367725 977 bp mRNA linear EST 21-JUL-2000
601217516F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586779 5',
mRNA sequence.
BE367725
BE367725.1 GI:9313153
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 977)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM8748 row: o column: 04
High quality sequence stop: 735.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/lab_host="DHL10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 275 a 288 c 226 g 188 t
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Query Match 40.1%; Score 636.6; DB 10; Length 977;
Best Local Similarity 95.9%; Pred. No. 7.3e-122;
Matches 707; Conservative 0; Mismatches 24; Indels 6; Gaps 5;
QY 649 TGAGCAGCTCAGTACTGCTCCCTCCAGCAGCTGCGCAAGTCAAGCTCAGCTCAGCG 708
Db 1 TGAGCAGCTCAGTACTGCTCCCTCCAGCAGCTGCGCAAGTCAAGCTCAGCTCAGCG 60
QY 709 TTGCTACCCGCCAGCAGCAGCAGCGGTGGCAAAACTTTGAGCCGCGGCGCCATTT 768
Db 61 TTGCTACCCGCCAGCAGCAGCAGCGGTGGCAAAACTTTGAGCCGCGGCGCCATTT 120
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Db 121 CAACAATCAACCCCTGCTCCATGCAAGGAGTGTCAAAATATCAAGGATGTACTCATCTCC 180
QY 829 AGGTTGAGCAGCTCCCTGCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATCTCC 888
Db 181 AGGTTGAGCAGCTCCCTGCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATCTCC 240
QY 889 TGACACCAAGGTACAGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 948
Db 241 TGACACCAAGGTACAGTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
QY 949 TCAGCTGTTTGTGAACACAGTGTGAAGTACACACAGCTCAGACAAACCCATAGAGAGG 1008
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Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3586779"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."
/lab_host="DHL10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 275 a 288 c 226 g 188 t
ORIGIN

Db	601	TTGAGACATCAGTGTGGGAGTGGACCAAGCAATGGGCATCCAGAGGAGAACTACAGTGACA	660
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Db	661	C--GCACCGGTCTGGACTCTGAGG-TCTTACTTCATATAGCAAGCTCGATATTAAC	717
QY	1366	CAAGCAAGTGGGAGAAA	1382
Db	718	CAGCAGTGGGAGAAACA	734
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LOCUS	BF136899	601783787F1 NCL_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4011837 5'	EST 24-OCT-2000
DEFINITION	BF136899	mRNA sequence.	
ACCESSION	BF136899		
VERSION	BF136899.1	GI:10975939	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 819)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9251 row: m column: 22 High quality sequence stop: 716.		
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	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MMV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
BASE COUNT	206 a 234 c 205 g 173 t		
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Query Match	39.6%;	Score 628.8; DB 12; Length 819;	
Best Local Similarity	93.2%;	Pred. No. 3.1e-120;	
Matches 713; Conservative	0; Mismatches 43; Indels 9; Gaps 5;		
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b	1	TCACAGTCTCTCAGCCAGAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTG	60
Y	505	GAGATACAACCTGGTTCCTC-CGTGACTCTGGGATGCCTGTCAAGGGCTACTTCCCTGAG	563
b	61	GAGATACAACCTGGTTCCTCTNGTCACTCTGGGATGCCTGTCAAGGGCTACTTCCCTGAG	120
Y	564	TCAGTGAAGTGAAGTTCGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCT	623
b	121	TCAGTGAAGTGAAGTTCGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCT	180
Y	624	CTCTGCAGTCTGGAGTCTACACTATGAGCAGCTCAGTGAAGTGTCCCTCCAGCACCTGG	683

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 1488 TCTCAGGTCTTAAGAGACACTGGCACCACCATATCCATGCTCCCTTGTATATAAAGCAT 1547
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 u34a01.x1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3661416 3',
 similar to SW-637_MOUSE P01866 IG GAMMA-2B CHAIN C REGION. ;, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BF148722 639 bp mRNA linear EST 29-DEC-2000
 u34a01.x1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3661416 3',
 similar to SW-637_MOUSE P01866 IG GAMMA-2B CHAIN C REGION. ;, mRNA
 sequence.

BF148722
 BF148722.1 GI:11030117
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 639)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Other ESTs: u34a01.y1
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Cloning Strategy: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

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 High quality sequence stop: 423.
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 Site 2: SalI; transgenic model WNT-1, expression driven by
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
 dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH
 122 a 140 c 171 g 205 t 1 others

BASE COUNT
 122 a 140 c 171 g 205 t 1 others

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 Matches 604; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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 1005 GAGGATTACACAGTACTATCCCGGTGGTCCAGCACCTCCCATCCAGCAGGACTGG 1064

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 270 ACCGCCACCT 211
 1365 ACAAGCAAGTGGGAGAAACAGATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAAA 1424
 210 ACAAGCAAGTGGGAGAAACAGATTCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAAA 151
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 30 CATCCAGCAAGGCTGGTACCATTGTA 1

RESULT 8
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 vx42e07.r1 Stragene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:1277892 5' similar to gb:S65761 IG GAMMA-2 CHAIN C REGION
 (HUMAN); gb:X67210 M.musculus rearranged immunoglobulin gamma 2b
 heavy (MOUSE);, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AA882246.1 GI:2991357
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 703)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Gessel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennop, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HHMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MG1:669692
 Putative full length read
 vector to vector length is 811

Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 271.

FEATURES
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/tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="SOUR (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site.1: EcoRI
; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo
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were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3',
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'
197 a 189 c 173 g 143 t 1 others

BASE COUNT
197 a 189 c 173 g 143 t

Query Match 35.3%; Score 560.4; DB 9; Length 703;
Best Local Similarity 91.8%; Pred. No. 4.7e-106;
Matches 647; Conservative 0; Mismatches 52; Indels 6; Gaps 5;

760 GGCCTATTTCAACATCAACCCCTCTCTCCATGCAAGGAGTGTCAAAATGCCAGCTC 819
|||||
1 GGCCTATTTCAACATCAACCCCTCTCTCCATGCAAGGAGTGTCAAAATGCCAGCTC 60
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820 CTAACTCCAGGCTGGACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 879
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61 CTAACTCCAGGCTGGACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
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880 TGATCTCCCTGACACCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
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121 TGATCTCCCTGACACCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
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940 AGCTCCAGATCAGCTGGT 999
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181 AGCTCCAGATCAGCTGGT 240
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1000 ATAGAGAGGATTACACAGTACTATCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1059
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241 ATAGAGAGGATTACACAGTACTATCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 299
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1060 ACTGGATGATGGCAGAGGATTCATATGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1119
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300 ACTGGATGATGGCAGAGGATTCATATGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 359
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1120 TCAGAGAGACCATCTCAAAATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1179
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360 TCAGAGAGACCATCTCAAAATTAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 419
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1180 CGCCACACAGAGAGT 1239
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420 CGCCACACAGAGAGT 479
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1240 TCACACCTGGAGACATCAGT 1298
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480 TCACACCTGGAGACATCAGT 539
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1299 AAGGACACCCACAGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1358
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540 AA-GACACCCACAGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 598
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1359 -ATGAACACAGCAAGT 1415
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599 AATGAACACAGCAAGT 658
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1416 GGTCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1460
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659 GTTCGGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 703
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RESULT 9
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BG084699 571 bp mRNA linear EST 26-JAN-2001
H3103H12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3103H12 5', mRNA sequence.
BG084699
BG084699.1 GI:12567263
EST.
mus mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 571)
Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka
, T.S., Carter, M.G. and Ko, M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set
Unpublished (2001)
Other ESTs: H3103H12-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://igun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3103 row: H column: 12
Seq primer: -21M13 Reverse
High quality sequence stop: 571
POLYA=No.

Location/Qualifiers
1. 571
/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="H3103H12"
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="clones arrayed from a variety of cDNA
libraries"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
, and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with Oligo(dT
)-Not primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A. 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."

BASE COUNT 138 a 176 c 136 g 121 t
ORIGIN

Query Match 35.28; Score 558.8; DB 12; Length 571;
Best Local Similarity 99.6%; Pred. No. 1e-105;
Matches 560; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 458 AGCCAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGATCAACTGG 517
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Db 10 AGCCAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGATCAACTGG 69
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518 TTCTCCCTGCTGCTGGGATGCTGGTCAAGGGCTTCTCCCTGAGTCAGTCAGTCGAC 577
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70 TTCTCTCTGCTGCTGGGATGCTGGTCAAGGGCTTCTCCCTGAGTCAGTCAGTCGAC 129
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578 TTGGAATCTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCCCTGAGTCG 637
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130 TTGGAATCTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCCCTGAGTCG 189
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638 ACTCTACACTATGACGACCTCAGTCAGTCGCTCCCTCCAGCAGCTGGCCAAAGTCAGACCGT 697
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190 ACTCTACACTATGACGACCTCAGTCAGTCGCTCCCTCCAGCAGCTGGCCAAAGTCAGACCGT 249
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698 CACCTGACGCTTGTCTACCCAGCAGCAGCAGCAGCAGCTGGTGACAAAAAATTTGAGCCAG 757
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758 CGGGCCCATTTTCAACAATCAACCCCTGCTCCATGCAAGGAGTGTCAAAATGCCAGC 817
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310 CGGGCCCATTTTCAACAATCAACCCCTGCTCCATGCAAGGAGTGTCAAAATGCCAGC 369
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818 TCCTTAACCTCGAGGGTGACCATCCGCTTTCATCTTCCCTCCAAATATCAAGGATGTACT 877
|||||
370 TCCTTAACCTCGAGGGTGACCATCCGCTTTCATCTTCCCTCCAAATATCAAGGATGTACT 429
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430 CATGATCTCCCTGACACCCCAAGGTCAGCTGTGGTGGTGGATGAGCGAGGATGACCC 489
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938 AGAGCTCCAGATCAGCTGGTGTGTAACAAGCTGGAAGTACACAGCTCAGACACAAAC 997
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490 AGAGCTCCAGATCAGCTGGTGTGTAACAAGCTGGAAGTACACAGCTCAGACACAAAC 549
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998 CCATAGAGGATTTACAAACAGT 1019
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550 CCATAGAGGATTTACAAACAGT 571

RESULT 10
BM243266/c
OCUS
DEFINITION
BM243266
BM243266.1 GI:17878536
EST.
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 552)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G.,
Taub, D., Longo, D.L., Keller, J., and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/c-kit-/Sca-1+) cDNA Library (Long)
Unpublished (2001).
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@ngsun.grc.nia.nih.gov
Plate: K0644 row: A column: 12
Seq primer: -21M13 Forward
High quality sequence stop: 552
POLYA=Yes.
Location/Qualifiers
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/strain="C57BL/6NCr"
/db_xref="niaEST:K0644A12-3"
/db_xref="taxon:10090"
/clone="K0644A12"
/clone_lib="NIA Mouse Hematopoietic Stem Cell"

(Lin-/c-kit-/Sca-1+) cDNA Library (Long)"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-kit-/Sca-1+)"
/dev_stage="Age approx. 10 weeks old"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research, Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Cancer Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]: 5'-pGACTAGTCTCAGATGCGAGCGCGCCCTTTT-3' from 1.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)." 170 g
BASE COUNT 107 a 125 c 150 g
ORIGIN
Query Match 34.3%; Score 544; DB 13; Length 552;
Best Local Similarity 99.1%; Pred. No. 1.2e-102;
Matches 547; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1018 GTACTATCCGGTGGTCCAGCACCCCTCCCATCCAGCACCAGGACTGGATGATGGCAAGG 1077
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Db 552 GTACTATCCGGTGGTCCAGTCCCTCCCATCCAGCACCAGGACTGGATGATGGCAAGG 493
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QY* 1078 AGTTCAATGCAAGGTCAACAACAAGACCTCCCATCCAGCACCAGGACTGGATGATGGCAAG 1137
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Db 492 AGTTCAATGCAAGGTCAACAACAAGACCTCCCATCCAGCACCAGGACTGGATGATGGCAAG 433
|||||
QY 1138 AAATTAAGGCTAGTCAGAGCTCCAGAGTATACATCTTCCCGCCACGACGAGCAGT 1197
|||||
Db 432 AAATTAAGGCTAGTCAGAGTCCACAAGTATACATCTTCCCGCCACGACGAGCAGT 373
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QY 1198 TGTCAGGAAGATGTGAGTCTCAGTCTCAGTTCCTGGTGGTTCACCCCTGGAGACATCA 1257
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Db 372 TGTCAGGAAGATGTGAGTCTCAGTCTCAGTTCCTGGTGGTTCACCCCTGGAGACATCA 313
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QY 1258 GTGTGGAGTGGACCAAGTGGGATACAGAGGAGAACTACAAGACACCGCAGTCC 1317
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Db 312 GTGTGGAGTGGACCAAGTGGGATACAGAGGAGAACTACAAGACACCGCAGTCC 253
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QY 1318 TGGACTCTGACGGTTCCTTCTCATATATAGCAGCTCAATATGAAAACAGCAAGTGGG 1377
|||||
Db 252 TGGACTCTGACGGTTCCTTCTCATATACAGAGCTCGATATAAAACAGCAAGTGGG 193
|||||
QY 1378 AGAAAACAGATTCCTTCTCATGCAAGCTGAGACAGAGGCTCTGAAAAATTTACTTACCTGA 1437
|||||
Db 192 AGAAAACAGATTCCTTCTCATGCAAGCTGAGACAGAGGCTCTGAAAAATTTACTTACCTGA 133
|||||
QY 1438 AGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGTCC 1497
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Db 132 AGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGTCC 73
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QY 1498 TAGAGACACTGGCACCCTATCCATGCTCCCTTGTATAAATAAGCAGTCCAGCAAGC 1557
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Db 72 TAGAGACACTGGCACCCTATCCATGCTCCCTTGTATAAATAAGCAGTCCAGCAAGC 13
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QY 1558 CTGGTACCATGT 1569


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/clone_lib="IMAGE:3417612"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
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was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Souares and M. Fatima Bonaldo."
103 a 123 c 149 g 172 t

BASE COUNT
ORIGIN
Query Match 33.8%; Score 536; DB 12; Length 547;
Best Local Similarity 99.1%; Pred. No. 5.6e-101;
Matches 539; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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1083 AATGCAAGGTCAACAAAGAGCTCCATCCATCCAGGAGAACCTCTCAAAATT 1142
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|||||
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1203 AGGAAGATGTCACTCTCAGTCTGCTGGTGGGCTTCAACCCCTGGAGACATCAGTGTG 1262
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367 AGGAAGATGTCACTCTCAGTCTGCTGGTGGGCTTCAACCCCTGGAGACATCAGTGTG 308
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1263 GAGTGGACCAAGCAATGGGCATACAGAGAGAACTACAGGAGACACCGCACCTCTGGAC 1322
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307 GAGTGGACCAAGCAATGGGCATACAGAGAGAACTACAGGAGACACCGCACCTCTGGAC 248
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1323 TCTGACGGTCTTACTTCATATATAGCAAGCTCAATATGAAACAAAGCAAGTGGAGAAA 1382
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247 TCTGACGGTCTTACTTCATATATAGCAAGCTCAATATGAAACAAAGCAAGTGGAGAAA 188
|||||
1383 ACAGATTCCTCTCATGCAAGCTGAGACAGAGGCTCTGAAAAATTTACTCTCTGAAGAG 1442
|||||
187 ACAGATTCCTCTCATGCAAGCTGAGACAGAGGCTCTGAAAAATTTACTCTCTGAAGAG 128
|||||
1443 ACCATCTCCCGGCTCCGGGTAATAGTACGACACCCACAAAGCTCTCAGGTCTTAAGA 1502
|||||
127 ACCATCTCCCGGCTCCGGGTAATAGTACGACACCCACAAAGCTCTCAGGTCTTAAGA 68
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1503 GACACTGGCACCACATATCCATGCTCCCTTGTATATAAAGATCCAGCAAGGCTGGT 1562
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1563 ACCA 1566
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7 ACCA 4

RESULT 13
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OCUS
DEFINITION
BF134589 530 bp mRNA linear EST 24-OCT-2000
601779503F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4007424 5',
mRNA sequence.
CROSSON
BF134589
ERSON
BF134589.1 GI:10973629
EYWORDS
EST.
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house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 530)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM9240 row: f column: 01
High quality sequence stop: 528.

Location/Qualifiers
1. 530
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/db_xref="taxon:10090"
/clone_lib="IMAGE:4007424"
/tissue_type="tumour, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 149 a 150 c 126 g 105 t
ORIGIN

Query Match 33.2%; Score 526.8; DB 12; Length 530;
Best Local Similarity 99.6%; Pred. No. 4.5e-99;
Matches 528; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 744 AAATTTGAGCCAGCGGGCCCATTTTCAACAATCAACCCCTGCTCCATGCAAGAGTGT 803
Db 1 AAATTTGAGCCAGCGGGCCCATTTTCAACAATCAACCCCTGCTCCATGCAAGAGTGT 60
QY 804 CACAATGCCAGCTCTTAACCTCGAGGGTGGACCATCCGCTTTCATCTTCCCTCAAT 863
Db 61 CACAATGCCAGCTCTTAACCTCGAGGGTGGACCATCCGCTTTCATCTTCCCTCAAT 120
QY 864 ATCAAGGATGTACTCATGATCTCCCTGACACCCCAAGTCACTGTGTGGTGGATGTG 923
Db 121 ATCAAGGATGTACTCATGATCTCCCTGACACCCCAAGTCACTGTGTGGTGGATGTG 180
QY 924 AGCGAGGATGACCCAGAGCTCCAGATCAGTCTGTTGTGAACAGTGGAAAGTACACACA 983
Db 181 AGCGAGGATGACCCAGAGCTCCAGATCAGTCTGTTGTGAACAGTGGAAAGTACACACA 240
QY 984 GCTCAGACACAAACCCATAGAGAGATTACAACTACTATCCGGGGTGGTCCAGCCCTC 1043
Db 241 GCTCAGACACAAACCCATAGAGAGATTACAACTACTATCCGGGGTGGTCCAGCCCTC 300
QY 1044 CCCATCCAGCACCAGGAGTGGATGATGCGGAGAGTTCAAATGCAAGGTCAACACAAA 1103
Db 301 CCCATCCAGCACCAGGAGTGGATGATGCGGAGAGTTCAAATGCAAGGTCAACACAAA 360
QY 1104 GACCTCCCATCACCATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGTCCA 1163
Db 361 GACCTCCCATCACCATCGAGAGAACCATCTCAAAAATTAAGGGCTAGTCAGAGTCCA 420
QY 1164 CAAGTATACATCTTTCGCGCCACCCAGCAGAGTGTCCAGGAAAGATGTCCAGTCTCACT 1223
Db 421 CAAGTATACATCTTTCGCGCCACCCAGCAGAGTGTCCAGGAAAGATGTCCAGTCTCACT 480
QY 1224 TGCTGGTCTGGGCTTCAACCCCTGAGACATCAGTGTGGAGTGGACAG 1273

Site_2: Sali; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH

BASE COUNT	271 a	275 c	214 g	179 t
ORIGIN				
Query Match	32.0%	Score 507.6;	DB 12;	Length 939;
Best Local Similarity	82.0%	Pred. No. 3.9e-95;		
Matches 628;	Conservative 0;	Mismatches 119;	Indels 19;	Gaps 3;

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Db	1	CTACACCTTCAGCAGCTCAGTGTCTCCCTCCAGCAGCTGCGCAAGTCAGACCGTCAC	60
QY	701	CTGACGCGTGTCTACCCAGCCAGCAGCAGCGTGGACAAAACCTTGAGCCGAGCGG	760
Db	61	CTGCAATGTGGCCACCCGCGAAGCAGCAGCGTGGACAAAACCTTGAGCCGAGCGG	120
QY	761	GGCCATTTCAACAATCAACCCCTGTCTCCATGCAAGAGGTGTCAAAATGCCAGCTCC	820
Db	121	GGCC-----ACAATCAAGCCCTGTCTCCATG-----CAAATGCCAGCACC	162
QY	821	TAACTCGAGGGTGGACCATCGTCTTCATCTTCCCTCAAATATCAAGGATGTACTCAT	880
Db	163	TAACTCTTGGGTGGACCATCGTCTTCATCTTCCCTCAAATATCAAGGATGTACTCAT	222
QY	881	GATCTCCCTGACACCCAGGTCACGTCGTGTGTGGTGGATGTGAGCGAGGATGACCCAGA	940
Db	223	GATCTCCCTGACCCCATGTCACATGTGTGGTGGATGTGAGCGAGGATGACCCAGA	282
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Db	283	TCTCCAGATCAGCTGTTCTGTAACAACGTGGAAGTACACAGCTCAGACACAAACCCA	342
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Db	343	TAGACAGATTACACAGTACTATCCGGTGTGTGAGCAGCCCTCCCATTCAGCAGGAA	402
QY	1061	CTGGATGAGTGCAGAGGAGTTCAATGCAAGTCAACACAAAGAGCTCCCATTCAGCAGG	1120
Db	403	CTGGATGAGTGCAGAGGAGTTCAATGCAAGTCAACACAAAGAGCTCCCATTCAGCAGG	462
QY	1121	CGAGAGAACCATCTCAAAATTAAGGGCTAGTCAGAGCTCCACAGTATACATCTTGCC	1180
Db	463	CGAGAGAACCATCTCAAAATTAAGGGCTAGTCAGAGCTCCACAGGATATGCTTGCC	522
QY	1181	GCCACAGCAGCAGTGTGTCCAGGAAGATGTCTAGTCTCAGTTCCTGCTGGTGGCTT	1240
Db	523	TCCACAGGAAGAGATGACTAAGAAAGCTCAGTCTGACCTGCATGGTCAGAGACTT	582
QY	1241	CAACCTGGAGACATCAGTGTGGAGTGACCAAGCAATGGCATACAGAGAGAACTACAA	1300
Db	583	CATGCTGAAGACATTTAGTGGAGTGGACCAACACGGGAAACAGAGCTAAACTACAA	642
QY	1301	GGACAGCAGCAGCTCTGGACTCTGACGGTCTTACTTATATATACAGAGCTCAATAT	1360
Db	643	GAACACTG-AACAGTCCGGGATTCGTGTTCTTACTTCTACGTACAGCAAGCTGAGAGT	701
QY	1361	GAATAACAAGAGTGGGAGAAACAGATTCTCTCTCATGCAAGCTG 1406	
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Search completed: June 24, 2003, 01:19:55
Job time : 2537.69 secs

result No.	Score	Query		DB	ID	Description
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1	919.8	57.9	8600	9	US-10-144-771-19352	Sequence 19352, A
2	795	50.1	1407	10	US-10-429-662-9	Sequence 9, Appli
3	795	50.1	1407	10	US-10-429-660-9	Sequence 9, Appli
4	781.2	49.2	1407	1	PCT-US02-02373-14	Sequence 14, Appl
5	774	48.7	1109	9	US-10-272-899A-81	Sequence 81, Appl
6	769.2	48.4	1109	9	US-10-272-899A-79	Sequence 79, Appl
7	768.6	48.4	1027	9	US-10-272-899A-21	Sequence 21, Appl
8	763.8	48.1	1027	9	US-10-272-899A-23	Sequence 23, Appl
9	670.6	42.2	1386	1	PCT-US02-34420A-21	Sequence 21, Appl
10	670.6	42.2	1386	1	PCT-US02-3533A-21	Sequence 21, Appl
11	670.6	42.2	1386	9	US-10-286-132A-21	Sequence 21, Appl
12	670.6	42.2	1386	9	US-10-281-479A-21	Sequence 21, Appl
13	670.6	42.2	1398	10	US-10-275-180A-21	Sequence 21, Appl
14	648.8	40.9	1392	10	US-10-384-933-8	Sequence 8, Appli
15	643.6	40.5	1673	9	US-10-342-887-1932	Sequence 1932, Ap
16	643.6	40.5	1673	12	PCT-US02-36107-53	Sequence 237, App
17	639	40.2	1410	1	US-10-292-088-53	Sequence 53, Appl
18	639	40.2	1410	10	US-10-292-088-53	Sequence 53, Appl
19	638.6	40.2	1430	5	US-09-848-832-1	Sequence 1, Appli
20	638.6	40.2	1430	10	US-10-225-108A-1	Sequence 1, Appli

77 AGTCACAGTACGCTCAGCAACAAACAGCCCATCGGTCTATCCACTGGGCCCTCGTGTG 136
503 TGGAGATACAACTGGTTCCTCGGTGACTCTGGGATGCTGTGTCAGGGCTACTTCCCTGA 562
137 TGGAGGTACAACTGGCTCCTCGGTGACTCTAGGATGCTGTGTCAGGGCTATTTCCCTGA 196
563 GTCAGTACTGCTGACTTGGAACTCTGGATCCCTGTCCAGAGCTGTGACACACTTCCAGC 622
197 GCCAGTACCTTGGCTGAACTCTGGCTCCTGTCCAGTGTGTGACACACTTCCAGC 256
623 TCTCCTGAGTCTGAGTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 682
257 TCTCCTGAGTCTGAGTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 316
683 GCCAAGTACAGCTCAGCTCAGCTGCTGCTCAGCCAGCAGCAGCAGCAGCTGAGCAA 742
317 GCCCAGCAGACCATCAGCTGCAATGTGGCCACCCGCGCAGAGCAGCAGCTGAGCAA 376
743 AAAAATTGAGCCAGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATCAAGAGTG 802
377 GAAAATTGAGCCAGAGTGCCCAT---AACACAGAACCCCTGTCTCCATCAAGAGTG 433
803 TCACAAATGCCAGCTCCTACCTCGAGGTGGAGCATCCGCTCTTCTATCTTCCCTCCAAA 862
434 TCCCCCATGGCAGCTCCAGACCTCTTGGGTGGACCATCCGCTCTTCTATCTTCCCTCCAAA 493
863 TATCAAGGTGTACTCATGATCTCCCTGACACCAAGTCAAGTGTGTGGTGGTGTG 922
494 GATCAAGGTGTACTCATGATCTCCCTGAGCCCATGTGTGCTGCTGCTGCTGCTG 553
923 GAGGAGGTGTACTCATGATCTCCCTGACACCAAGTCAAGTGTGTGGTGGTGTG 982
554 GAGGAGGTGTACTCATGATCTCCCTGAGCCCATGTGTGCTGCTGCTGCTGCTG 613
983 AGCTCAGACAAACCCATAGAGAGGATTACACAGTACTTCCCGGTGTGCTGCTG 1042
614 AGCTCAGACAAACCCATAGAGAGGATTACACAGTACTTCCCGGTGTGCTGCTG 673
1043 CCCCATCCAGCAGCAGCTGAGTGTGCTGAGAGGATTCAATGCAAGTGTGCTGCTG 1102
674 CCCCATCCAGCAGCAGCTGAGTGTGCTGAGAGGATTCAATGCAAGTGTGCTGCTG 733
1103 AGACTCCCATCCATCCAGAGAACCATCTCAAAATTAAGGGCTAGTTCAGAGCTCC 1162
734 AGCTCCTCCATCCCATCCAGAGAACCATCTCAAAATTAAGGGCTAGTTCAGAGCTCC 793
1163 ACAAGTATACATCTTGGCCGACACAGCAGAGCTGTGCTCAGGAAAGATGTGCTGCTC 1222
794 ACAGGTATATGCTTGGCTCCACAGCAGAGAGATGACTAAGAAAGTGTGCTGCTGCTG 853
1223 TTGCTGCTGCTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1282
854 CTGATGATCAGAGCTTCTTACCTGCGGAAATGTGCTGAGTGGAGCAGCAATGGCG 913
1283 TACAGAGGAGAACTACAGAGCAGCAGCAGCTGCTGAGTGTGCTGAGTGTGCTGAGT 1342
914 TACAGAGGAGAACTACAGAGCAGCAGCAGCTGCTGAGTGTGCTGAGTGTGCTGAGT 973
1343 ATATAGAGCTCAATATGAAACAGCAGTGGGAGAAACAGATTTCTTCTATGCAA 1402
974 GTACAGCAGCTCAGAGTACAAAGAGCAGTGGGAGAAAGAGTCTTTTTCGCTGCTC 1033
1403 CGTGAGAGCAGGCTGTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1462
1034 AGTGGTCCAGAGGGTCTGCACAACTACCTTACAGTAAAGACCATCTCCCGGTCTCGGG 1093
1463 TAAATGAGCT 1472
1094 TAAATATCT 1103

; Sequence 79, Application US/10272899A
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Key
; TITLE OF INVENTION: MONOCLONAL DNA CASSETTE MOLECULES,
; TITLE OF INVENTION: MONOCLONAL CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MP101-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 1109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin cassette sequence
; OTHER INFORMATION: Leader-Mu_FcR1I_61
US-10-272-899A-79

Query Match 48.4%; Score 769.2; DB 9; Length 1109;
Best Local Similarity 84.9%; Pred. No. 2,1e-191;
Matches 874; Conservative 0; Mismatches 153; Indels 3; Gaps 1;
QY 443 AGTCACAGTCTCCTCAGCAACAAACAGCCCATCGGTCTATCCACTGGGCCCTCGTGTG 502
Db 77 AGTCACAGTCTCCTCAGCAACAAACAGCCCATCGGTCTATCCACTGGGCCCTCGTGTG 136
QY 503 TGGAGATACAACTGGTTCCTCGGTGACTCTGGGATGCTGTGTCAGGGCTACTTCCCTGA 562
Db 137 TGGAGGTACAACTGGCTCCTCGGTGACTCTAGGATGCTGTGTCAGGGCTATTTCCCTGA 196
QY 563 GTCAGTACTGCTGACTTGGAACTCTGGATCCCTGTCCAGAGCTGTGACACACTTCCAGC 622
Db 197 GCCAGTACCTTGGCTGAACTCTGGCTCCTGTCCAGTGTGTGACACACTTCCAGC 256
QY 623 TCTCCTGAGTCTGAGTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 682
Db 257 TCTCCTGAGTCTGAGTCTACATATGAGAGCTCAGTGTGCTCCCTCCAGCAGCTG 316
QY 683 GTCAGTACTGAGTCTGAGTCTGAGTGTGCTGAGTGTGCTGAGTGTGAGCAA 742
Db 317 GCCCAGCAGACCATCAGTGTGCTGAGTGTGCTGAGTGTGAGCAA 376
QY 743 AAAAATTGAGCCAGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATCAAGAGTG 802
Db 377 GAAAATTGAGCCAGAGTGCCCAT---AACACAGAACCCCTGTCTCCATCAAGAGTG 433
QY 803 TCACAAATGCCAGCTCCTACCTCGAGGTGGAGCATCCGCTCTTCTATCTTCCCTCCAAA 862
Db 434 TCCCCCATGGCAGCTCCAGACCTCTTGGGTGGACCATCCGCTCTTCTATCTTCCCTCCAAA 493
QY 863 TATCAAGGTGTACTCATGATCTCCCTGACACCAAGTCAAGTGTGTGGTGGTGTG 922
Db 494 GATCAAGGTGTACTCATGATCTCCCTGAGCCCATGTGTGCTGCTGCTGCTGCTG 553
QY 923 GAGGAGGTGTACTCATGATCTCCCTGAGCAGCTGAGTGTGCTGAGTGTGAGTGTGAGTGTG 982
Db 554 GAGGAGGTGTACTCATGATCTCCCTGAGCAGCTGAGTGTGCTGAGTGTGAGTGTGAGTGTG 613
QY 983 AGCTCAGACAAACCCATAGAGAGGATTACACAGTACTTCCCGGTGTGCTGCTG 1042
Db 614 AGCTCAGACAAACCCATAGAGAGGATTACACAGTACTTCCCGGTGTGCTGCTG 673
QY 1043 CCCCATCCAGCAGCAGCTGAGTGTGCTGAGAGGATTCAATGCAAGTGTGCTGCTG 1102

143 TCAGTAGCTATGTAATGCTTGGGTTCCGAGACTCCGGAGNAGAGGCTGGAGTGGGTCG 202
235 GAGTGATATGGAGTGGTG---GAGACACAGACTATATGACGCTTTCATATCCAGACTGA 291
203 CAACCAATAGTAGTGGTGGTAGTACACCTACTATCCAGACAGTGTGAAGGGGGGATTC 262
292 GCATCAGCAGGACAATTCGAAGAGCCAACTCTCTTTAAATGAACAGTCTCGAGCTA 351
263 CCATCTCCAGAGACAATGCCAGNACACCCTGTACCTGCAAAAGAGCAGTCTGAGGTCG 322
352 CTGACAGAGCATATATTTACTGTGCCAGAAATAGAGGGATATTTACTATGATTTCACTT 411
323 AGGACAGGCCATGATTTACTGTGCAAGACGGGG-----GGACTCTATGA 367
412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTACCGGCTCTCTCAGCCAAACACAC 471
368 TTAGCAGGACTACTGGGGCAAGGCCACCACTCTCAGAGTCTCTCAGCCAAACGAC 427
472 CCCATCAGTCTATCCACTGCCCTGGTGTGGAGATACAACTGGTCTCCGTGACTC 531
428 CCCATCTGTCTATCCACTGGCCCTGGATCTGTGCCAAACTAACTCCATGTGACCC 487
532 TGGATGCTGCTCAAGGGCTACTTCCCTCAGTCACTGACTGTGACTTGGAACTCTGGAT 591
488 TGGATGCTGCTCAAGGGCTATTTCCCTGAGCCAGTACAGTACCTGGAACCTCTGGAT 547
592 CCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCTGAGCTGTGAGTCTGACATATGA 651
548 CCCTGTCCAGGGTGTGCACACCTTCCAGCTCTCTGAGCTGTGAGTCTGACATCTGA 607
652 GCAGCTCAGTGTGCTCCCTCCAGCAGCTGGCCAGTCAACAGCTGACCTGACGAGTGG 711
608 GCAGCTCAGTGTGCTCCCTCCAGCAGCTGGCCAGCAGGAGCTGACCTGACGAGTGG 667
712 CTCACCCAGCAGCAGCAGCAGCTGGGAGCAAACTTTGAGCCAGCGGGCCATTTCAA 771
668 CCCACCCGCGCAGCAGCAGCAGCTGGGAGCAAACTTTGAGCCAGGAGTGTGGTGA 727
772 CAATCAACCCCTGCTCTCCTCAGCAGGAGTGTCAAAATGCCAGCTCTCAACCTCGAGG 831
728 AGCCTGCTATG-----TACAGTCCCGAG 751
832 GTGACCAATCCGCTTCTATCTCCCTCCAAATATCAAGGATGTACTATGATCTCCCTGA 891
752 AAGTATCATCTGCTTCTATCTCTCCCCCAAGGCCCAAGGATGTGCTACCATTACTCTGA 811
892 CACCAAGGTCAGTGTGCTGGTGGTGTGAGCGAGGATGAGCCAGCAGCTCCAGATCA 951
812 CTCCTAAGGTCAGTGTGCTGGTGGTGTGAGCATCAGCAAGGATGATCCGAGGTCAGTTC 871
952 GCTGTTTGTGAACAACCTGGAAGTACACAGCTTCAGACACAAACCCATAGAGAGATT 1011
872 GCTGTTTGTGATGATGTGAGGTCACACAGCTTCAGCGCAACCCCGGGAGGAGCAGT 931
1012 ACAACAGTACTATCCGGTGGTGTGAGCAGCTCCCTCCCATCCAGCAGGAGTGGTGA 1071
932 TCACAGCAGCTTTCGCTCAGTCACTGAGTTCACCTATGATGATGATGATGATGATGATG 991
1072 GCAAGGATTCAAATGCAAGGTCACACAAAGACCTCCCATCACCCTCCAGAGAACCA 1131
992 GCAAGGATTCAAATGCAAGGTCACACAGTGTGAGTTCCTCCCTCCCTCCAGAGAACCA 1051
1132 TCTCAAAATTAAGGGCTAGTCAAGCTTCCACAGTATACATCTTGGCCGACCCAGCAG 1191
1052 TCTCCAAACCAAGGAGAGCCGAGAGGTCACAGGTCACAGGTCACAGGTCACAGGTCAC 1111
1192 AGCAGTGTGCAAGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1251
1112 AGCAGTGTGCAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1171
1252 ACATCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1311

Db 1172 ACATTACTGTGGAGTGGCAGTGGGAATGGGCGAGCCAGCGAGAACTACAAGAACACTCAGC 1231
QY 1312 CAGTCTGGGACTCTGACGGTCTTACTTATATATAGCAAGCTCAATATGAAACAGCA 1371
Db 1232 CCATCATGGACACAGATGGCTTACTTCTGCTACAGCAAGCTCAATGTGCAAGAGAGCA 1291
QY 1372 AGTGGGAGAAAACAGATTCCTTCTCATGCAACGTCGACACAGAGGGTCTGAAAATTA 1431
Db 1292 ACTGGAGGAGGAAATACTTTCACCTGCTCTGTGTACATGAGGGCTGCAACCAACC 1351
QY 1432 ACCTGAGAGAGACCTCTCCGGTCTCCGGTAA 1466
Db 1352 ATACTGAGAGAGCCTCTCCACTCTCTCTGATAA 1386
RESULT 10
PCT-US02-35333A-21
; Sequence 21, Application PC/TUS0235333A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085,0029P2
; CURRENT APPLICATION NUMBER: PCT/US02/35333A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Descriptive of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
PCT-US02-35333A-21

Query Match 42.2%; Score 670.6; DB 1; Length 1386;
Best Local Similarity 69.4%; Pred. No. 1.8e-165;
Matches 982; Conservative 0; Mismatches 379; Indels 54; Gaps 3;
QY 55 TCTGCTGTGATGATCCCAAGCTGTGCTTATCCAGGTGCAGCTGAGCAGTCCAGGAC 114
Db 23 TTTTCTGCTGCTCTTTTAAAGGTGTCAGGTGTAAGTGTGCTGCTGAGTCTGGG 82
QY 115 CTGGCTAGTGCAGCCCTCAGACAGCTGTCCATCCTCAGTGTGCTGCTGCTGCTGCT 174
Db 83 GAGGCTTAGTGAAGCTGTGAGGTCCTCCGAACTCTCTGTCGACGCTTGAATCACT 142
QY 175 TAACTAGTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 234
Db 143 TCAGTGTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 202
QY 235 GAGTGTGATGAGTGGTG---GAGACACAGACTATAATGCACTTTCATATCCAGACTGA 291
Db 203 CAACCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 262
QY 292 GCATCAGCAGGAGCAATTCACAGAGCAACTCTTCTTTAAATGACACTCTGCGAGCTA 351
Db 263 CCATCTCCAGAGACAATGCAAGAACCCCTGTACTGTCAAAATGAGCAGTCTGAGTCTG 322
QY 352 CTGACACAGCCATATATTTACTGTGCGAGAAATAGAGGGATATTTTACTATGATTTCACTT 411

668 CCCACCCGCCAGCAGCACCAAGGTGGACAGAAAATTTGTGCCAGGGATTTGGTTGTA 727
772 CAATCAACCCCTCTCTCCATGCAAGAGGTGTACAAAATGCCAGCTCTAACTCGAGG 831
728 AGCCTTGCCATATG-----TACAGTCCCAG 751
832 GTGGACATCCCT 891
752 AAGTATCATCT 811
892 CACCAAGGTCACTGT 951
812 CTCTTAAGGTCACTGT 871
952 GCTGT 1011
872 GCTGT 931
1012 ACAACAGTACTATCCGGGT 1071
932 TCAACAGCAGCTTTCCGCTCAGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
1072 GCAAGGAGTTCAATGTCAAGGTCAACAGAGTCAACAGAGTCAACAGAGTCAACAGAGTCA 1131
992 GCAAGGAGTTCAATGTCAAGGTCAACAGAGTCAACAGAGTCAACAGAGTCAACAGAGTCA 1051
1132 TCTCAAAATTAAGGGT 1191
1052 TCTCAAAATTAAGGGT 1111
1192 AGCAGT 1251
1112 AGCAGT 1171
1252 ACATCAGT 1311
1172 ACATCAGT 1231
1312 CAGTCTGT 1371
1232 CCATCATGT 1291
1372 AGTGGGAAACAGATTCCT 1431
1292 ACTGGGAGGAGGAAATTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1351
1432 ACCTGAAGAACAGCATCTCCGGTCTCCGGGTAAA 1466
1352 ATACTGAGAAGAGCCTCTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1386

RESULT 13
Sequence 21, Application US/10275180A-21
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
FILE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002905
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 1398
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note =

OTHER INFORMATION: Synthetic Construct
US-10-275-180A-21

Query Match 42.2%; Score 670.6; DB 10; Length 1398;
Best Local Similarity 69.4%; Pred. No. 1.8e-165;
Matches 982; Conservative 0; Mismatches 379; Indels 54; Gaps 3;

QY 55 TCCTGCTGTGTGACATCCCAAGCTGTCTCTATCCAGGTGACAGTCAAGCAGTCAAGAC 114
Db 23 TTTTCTCTGTCTCTGTCT 82
QY 115 CTGGCCTAGTGCAGCCTCTACAGAGCTGTCCACTCAGCTCAGCTCAGCTCTCTCTCTCTCT 174
Db 83 GAGGCTTAGTGAAGCCTGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
QY 175 TAATAGCTATGTGTACACTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 234
Db 143 TCAGTAGCTATGTAAATGTCT 202
QY 235 GAGTGATATGGAGT 291
Db 203 CAACCAATTAGT 262
QY 292 GCATCAGCAAGGACAATTCAGAGGCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 351
Db 263 CCATCTCCAGAGCAATGCAAGACCCCTGTACCTGTGCAATGAGCAGTCTCAGGTCTG 322
QY 352 CTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATATGATTTTCACTT 411
Db 323 AGGACACGGCCATGTATTACTGTGCAAGCGGG-----GGACTCTATGA 367
QY 412 ATGCCATGAGTACTTGGGTCAAGAACTCTAGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 471
Db 368 TTACGACGGACTACTGGGGCAAGGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
QY 472 CCCCATCACTCTATCCACTTGGGCTGGGTGTGGAGATACAACTGGTTCCTCGTCACTC 531
Db 428 CCCCATCTCTCTATCCACTTGGGCTGGGTGTGGAGATACAACTGGTTCCTCGTCACTC 487
QY 532 TGGGATGCTGTCAAGGGCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 591
Db 488 TGGGATGCTGTCAAGGGCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 547
QY 592 CCTGTGCCAGCTGTGCACT 651
Db 548 CCTGTGCCAGCTGTGCACT 607
QY 652 GCAGTCTAGTACTTCT 711
Db 608 GCAGTCTAGTACTTCT 667
QY 712 CTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 771
Db 668 CCCACCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 727
QY 772 CAATCAACCCCT 831
Db 728 AGCCTTGCCATATG-----TACAGTCCCAG 751
QY 832 GTGGACATCCCT 891
Db 752 AAGTATCATCT 811
QY 892 CACCAAGGTCACTGT 951
Db 812 CTCTTAAGGTCACTGT 871
QY 952 GCTGT 1011
Db 872 GCTGT 931
QY 1012 ACAACAGTACTATCCGGGT 1071

Db 1115 AGGAGCAGATGGCCAGGATAAAGTCAGTCGACCTGCATGATACAGAGACTTCTCCCTG 1174
QY 1249 GAGACATAGTGGAGTGAGCCAGCAATGGGCATACAGAGGAACTACAAGACACCG 1308
Db 1175 AAGACATTAAGTGGAGTGAGTGAATGGGAGCCAGCGGAGAACTACAAGAACACTC 1234
QY 1309 CACCACTCTGACACTGACGGTCTTACTTTCATATATAGCAAGCTCAATATGAAACAA 1368
Db 1235 AGCCCATCATGAACACGATGGCTCTTACTTGTCTACAGCAAGCTCAATGTGCAAGA 1294
QY 1369 GCAAGTGGGAGAAACAGATTCTTCTCATGCAAGCTGAGACACAGAGGTCTGAAANA 1428
Db 1295 GCACTAGGAGCAGCAAAATCTTACCTGCTGTGTATCATGAGGCGCTGCAACACC 1354
QY 1429 ACTACTGAAGAAGACCACTCTCCGGCTCTCCGGTAAA 1456
Db 1355 ACCATACTGAGAAGACCTCTCCCACTCTCCGGTAAA 1392

RESULT 15
US-10-342-887-1932
; Sequence 1932, Application US/10342887
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1932
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1932

Query Match 40.5%; Score 643.6; DB 9; Length 1673;
Best Local Similarity 66.3%; Pred. No. 2.4e-156;
Matches 1021; Conservative 0; Mismatches 479; Indels 40; Gaps 5;

Y 55 TCTGCTGGTGCATATCCCAAGCTGTGCTCTATCCAGGTGCAGTGAAGCAGTCAAGAC 114
b 1115
Y 88 TTTTCCCTGCTGCTCTTTAAGAGGTGTCAGGTGCAGTGGTGGAGTCTGGGG 147
b 1115
Y 115 CTGCTAGTGCAGCCCTACAGAGCCTGTCCATCAGTGCACAGTCTCTGTTCTCAT 174
b 148 GAGCGTGGTCCAGCTGGGAGTCCCTGAGACTCTCTGTGCGAGCTCTGGATTCACT 207
Y 175 TAATAGCTATGTTGACAGTGGTTCGTAGCTCCAGGAAAGGGTCTGAGTGGCTGG 234
b 208 TCAGTAATATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGG 267
Y 235 GAGTGATATGAGTGGGAGACACAGACTATATGAG---CTTTCATATCCAGACTGA 291
b 268 CAGCTATGATGATGATGAGTGAAGTAAATAACTATGAGACTCCGTGAAGGGCCGATTCA 327
Y 292 GCATCAGCAAGGCAATTCGAAGACCAACTCTTCTTTAAATGAACAGTCTGGAGCTA 351
b 328 CCATCTCCAGAGCAATTCGAAGAACACAGTGTGTATATGCAAAATGAACAGCCTGAGCGC 387
Y 352 CTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGATATTACTA----- 400

Db 388 AGGACACGGCTGTATATTGTGCGAGAGAGGCTCGTGGGTACGATATACCTGCTGA 447
QY 401 -TGATTTCATTATGCGATGAGTACTTGGGTCAAGAACTCAGTCAACGCTCTCTCAG 459
Db 448 CTACTATCGGATATCTTGTACTTACTTGGGGCAGGAACTTGGTCACTCTCTCAG 507
QY 460 CCAAAACAAACACCCCATCATGCTATCCACTGCGCCCTGGGTGGAGATACAACTGTT 519
Db 508 CTTCCACCAAGGCCCATCGGTCTTCCCTGCGACCCCTCTCCAAAGAGACCTCTGGG 567
QY 520 CTTCCCTGATCTTGGATGCTGCTCAAGGGCTACTTCCCTGAGTCACTGACTGTGACTT 579
Db 568 GCACACGGCCCTGGCTGCTGCTCAAGGACTACTTCCCGAAGCGGTGACGGTGTCTG 627
QY 580 GGAACCTCTGATCCCTGCTCCAGCAGTGTGCACACTTCCAGCTCTCTCTCAG---TCTG 636
Db 628 GGAACCTCAGCGCCCTGACGAGCGGTGCACACTTCCGGCTCTCTTACACTCTCAG 687
QY 637 GACTCTACACTATGACGAGTCACTGACTGTCTCCCTTCCAGACCTCTGGCCAAAGTCAAGC 696
Db 688 GACTCTACTCTCCCTCAGCAGCGTGGTGACGCTGCTCCCTCCAGCAGCTTGGGCACCGACCT 747
QY 697 TCACCTGACGAGTGTCTCACCAGCGCAGCAGCAGCAGCGTGGACAAAAACTTTGAGCCCA 756
Db 748 ACATCTGCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAGAGAGTGTGAGCC-- 805
QY 757 GCGGGCCCATTTCAACAATCAACCCCTGTCTCCATGCAAGGAGTGTCAAAATGCCAG 816
Db 806 -----CAATCTGTGACAAACTCACACATCCACACCTGCCAG 846
QY 817 CTCCTAACCTCGAGGTGAGCCATCGTCTTCTATCTTCCCTCCAAATATCAAGGATGTAC 876
Db 847 CACCTGAATCTCTGGGGGACCGTCACTTCTCTTCTCCCAAAACCAAGGACACCC 906
QY 877 TCATGATCTCCCTGACACCCAGGTGACGTGTGTGGTGTGATGTGACGAGGATGACC 936
Db 907 TCATGATCTCCCGGACCCCTGAGGTACATGGTGGTGGACGTGACCGACGAGAC 966
QY 937 CAGAGCTCCAGATCAGCTGTTTGTGAACAAGCTGGAAGTACACAGCTCAGACACAAA 996
Db 967 CTGAGGTCAAGTTCACTGAGTGTGAGCGGTGAGGTGATATGCCAAGACAAAGC 1026
QY 997 CCCATAGAGAGGATTACACAGTACTATCCGGGTGTCAGCACCTCCCTCCCATCCAGCAC 1056
Db 1027 CCGCGGAGGAGCAGTACACAGCAGTACCGTGTGTCAGCTCTCTCAGCTCTCTGCACC 1086
QY 1057 AGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGTCAACAAAGACCTCCCATCAC 1116
Db 1087 AGGACTGGCTGAATGGCAAGGAGTACAAAGTGTCAAGTCTCCAAAGAGCCCTCCAGCC 1146
QY 1117 CCATCGAGAGAACCATCTCAAAATTAAGGGCTAGTCAAGCTCCAAAGTATACATCT 1176
Db 1147 CCATCGAAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACC 1206
QY 1177 TGCCGCCACACGAGCAGCAGTGTGTCAGGAAAGATGTAGTCTCACTTGCCTGCTGGTGG 1236
Db 1207 TGCCGCCATCCCGGAGGAGATGACCTLGAACAGGTGAGCTGAGCTGCTCTGCTGGTCAAG 1266
QY 1237 GCTTCAACCTCGAGACATCAGTGTGAGTGAGTGCAGCAATGGGCATACAGAGGAGAACT 1296
Db 1267 GCTTCTATCCAGCAGCATCGCGTGTGAGTGGAGAGCAATGGGCGCGGAGAACAACT 1326
QY 1297 ACAGGACACCGCAGCAGTCTCTGGACTCTGAGGTTCTTACTTCTATATATAGCAAGCTCA 1356
Db 1327 ACAAGACCAAGCTTCCCGTGTGACTCCGACGGCTCTCTTCTCTCTATAGCAAGCTCA 1386
QY 1357 ATATGAAACAGCAAGTGGAGAACTCAGATTCTCTCATGCAAGCTGAGACAGGAG 1416
Db 1387 CCGTGGACAAGAGCAGGTGCGCAGCAGTGTCTCTCATGCTCTCTCTGATGATGAGG 1446
QY 1417 GTCTGAAAAATTAATCTACCTGAGAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGC 1476

1447 CTCTGCAACACACTACACGAGAGAGCCCTCTCCCTGTCCCCGGGTAAATGAGTGGAC 1506
1477 ACCCACAAGCTCTCAGGTCCCTAAGAGACACTGGCACCACATATCCATGCATCCCTTGTAT 1536
1507 GGCCGGCAGC-CCCCGCTCCCCGGGTCTCGCGTCCGACGAGGATGCTTGGCACGTAC 1565
1537 AAATAAAGCATCCAGCAAGCCTGGTACCATGTAAAAAA 1576
1566 CCGTCTACATCTCCAGGACCCAGCATGGAAATAA 1605

Search completed: June 24, 2003, 01:56:47
Job time : 1276.84 secs

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MM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 18:59:37 ; Search time 3974.64 Seconds
(without alignments)
10045.255 Million cell updates/sec

Title: US-09-770-916-1
Perfect score: 1588
Sequence: 1 ccacctcttctcatagc.....taaaaaaaaaaaaaaaaaaa 1588

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues 495822208
Total number of hits satisfying chosen parameters:

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Maximum DB seq length: 2000000000

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3	1081.2	68.1	1365	25	US-09-653-755A-1 Sequence 1, Appli
4	963	60.6	1645	3	US-07-904-074A-3 Sequence 3, Appli
5	940.8	59.2	1570	3	US-07-743-329-6 Sequence 6, Appli
6	940.8	59.2	1570	7	US-08-303-569-6 Sequence 6, Appli
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22 740.8 46.6 1676 31 US-09-815-837-82 Sequence 82, Appl
23 737.8 46.5 6729 24 US-09-629-4308-4 Sequence 4, Appl
24 684.8 43.1 2053 1 PCT-US01-09616-63 Sequence 63, Appl
25 684.8 43.1 2053 1 US-09-815-837-63 Sequence 63, Appl
26 684.8 43.1 2059 1 PCT-US01-09616-66 Sequence 66, Appl
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28 674.6 42.2 1398 8 US-08-480-120-1 Sequence 1, Appl
29 670.6 42.2 1398 1 PCT-US01-14151-21 Sequence 21, Appl
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32 659 41.5 1610 30 US-09-760-479-190 Sequence 190, Appl
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35 654.6 41.2 1798 1 PCT-US00-05883-230 Sequence 230, Appl
36 654.6 41.2 1798 34 US-09-925-299-230 Sequence 230, Appl
37 653.6 41.2 1787 24 US-09-637-886-992 Sequence 992, Appl
38 653.6 41.2 1787 25 US-09-652-125A-9483 Sequence 9483, Appl
39 653.6 41.2 1787 25 US-09-652-127-9399 Sequence 9399, Appl
40 653.6 41.2 1787 27 US-09-698-010-15669 Sequence 15669, A
41 653.6 41.2 1787 27 US-09-699-999-7476 Sequence 7476, Appl
42 653.6 41.2 1787 28 US-09-710-281-5790 Sequence 5790, Appl
43 653.6 41.2 1787 29 US-09-726-174-5933 Sequence 5933, Appl
44 653.6 41.2 1787 29 US-09-726-211-1568 Sequence 1568, Appl
45 651.8 41.0 1567 14 US-09-049-672-17 Sequence 17, Appl

ALIGNMENTS

SULT 1

-09-770-916-1

Sequence 1, Application US/09770916

GENERAL INFORMATION:

APPLICANT: Frank, Dara W.

APPLICANT: Wiener-Kronish, Jeannine

APPLICANT: Yahr, Timothy L.

APPLICANT: Sava, Teiji

APPLICANT: Fritz, Robert B.

TITLE OF INVENTION: Method of and compositions for immunization with the

FILE OF INVENTION: pseudomonas V antigen

FILE REFERENCE: 650053.91487

CURRENT APPLICATION NUMBER: US/09/770,916

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 09/448,339

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: 60/109,952

PRIOR FILING DATE: 1998-11-25

PRIOR APPLICATION NUMBER: 60/126,794

PRIOR FILING DATE: 1999-03-30

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1588

TYPE: DNA

ORGANISM: mouse

FEATURE:

NAME/KEY: CDS

LOCATION: (33)..(1466)

NAME/KEY: sig_peptide

LOCATION: (33)..(89)

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OTHER INFORMATION: FR1

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Sequence 1, Application US/09653755A
GENERAL INFORMATION:
APPLICANT: Eislinger, Dominic P.
APPLICANT: Stiles, Lynn
APPLICANT: LaMarche, Arthur
APPLICANT: Jelinek, Thomas
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins
FILE REFERENCE: 724650-3
CURRENT APPLICATION NUMBER: US/09/653,755A
CURRENT FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1365
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:cDNA for heavy
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2Y 1468 GA 1469
Db 1364 GA 1365

RESULT 4

IS-07-904-074A-3
: Sequence 3, Application US/07904074A
: GENERAL INFORMATION:
: APPLICANT: John E. Shively
: APPLICANT: Rainer Fischer
: APPLICANT: Anna Wu
: APPLICANT: Roy Paxton
: APPLICANT: Y.H. Joy Yang
: TITLE OF INVENTION: Chimeric Anti-CEA Antibody
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: City of Hope
: STREET: 1500 East Duarte Road
: CITY: Duarte
: STATE: California
: COUNTRY: United States of America
: ZIP: 91010-0269
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3M Double Density 5 1/4" diskette
: COMPUTER: Wang PC
: OPERATING SYSTEM: MS-DOS (R) Version 3.30
: SOFTWARE: Microsoft (R)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/904,074A
: FILING DATE: 19920615
: CLASSIFICATION: 530

PRIOR APPLICATION DATA: None
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: None
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 785-6938
TELEFAX: (202) 785-5351
TELEX: 440087 LM WSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1645
TYPE: NUCLEIC ACID
STRANDEDNESS: Single Stranded
TOPOLOGY: Unknown
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: Not Applicable
ANTI-SENSE: Not Applicable
FRAGMENT TYPE: Not Applicable
ORIGINAL SOURCE: Synthetically Prepared
IMMEDIATE SOURCE: Synthetically Prepared
POSITION IN GENOME: None
FEATURE: None
PUBLICATION INFORMATION: None

IS-07-904-074A-3

Query Match 60.6%; Score 963; DB 3; Length 1645;
Best Local Similarity 77.6%; Pred. No. 6.8e-226;
Matches 1215; Conservative 0; Mismatches 320; Indels 30; Gaps 3;
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70 CACCTCACCATGAATTCGGGTTTCAGCCTGATTTTCCTTGCTTTGTTTAAAGGTGTC 129
84 CTATCCAGGTGACGCTGAAGCAGCTCAGGACCTGGCCTAGTGCAGCCCTCACAGGCCTG 143

Db 130 CAGTGTGAAGTCAAGCTGGTGGAGTCTGGGGGAGGCTTTGTGAAGGCTGGAGGTCCTCTG 189
QY 144 TCATCATCCTGCACAGTCTCTGGTTCTCTCAATTAACATAGTATGGTGTACACTGGGTTCTG 203
Db 190 AAATCTCTCTGTCGACCTCCCGATTCATTTTCAGTAGTTATGCCATGCTCTTGGGTTCCG 249
QY 204 CAGTCTCCAGGAAAGGCTCTGGAGTGGCTGGGAGTCATATGAGTGGTGGAGACACAGAC 263
Db 250 CAGACTCCAGAGAGAGGCTGGAGTGGGTCGATCCATTTAGTAGTGGTATCACTTC 309
QY 264 TATAATGCAGCTTTTCATATCCAGACTGAGCATCAGCAAGGACAAATTCACAGCCAACTC 323
Db 310 TATGTAGACAGTGTGAAGGCGGATTCACCGTCTCCAGAGACAATGCCAGGACATCTCTG 369
QY 324 TTTCTTTAAATGAACAGTCTGCGAGCTACTGACAGCCATATATTACTGTGCCAGAAAT 383
Db 370 TACCTGCAATGAGCAGTCTGAGGTCCTGAGGACACGCGCATATTTACTGTGCAAA --- 426
QY 384 AGAGGGGATATTTACTATGATTTTCACTTATGCCATGGAGTACTGGGGTCAAGAACCTCA 443
Db 427 -----ATCGACTACTACGAGGAGGGGATTTGGTTACTGGGGCCAAAGGACTCTG 477
QY 444 GTCACGCTCTCTCAGCCAAACAAACACCCCATCAGTCTATCCACTGCCCTGGGTGT 503
Db 478 GCCACTGCTCTGACAGCAAAACAAAGCCCATCGGTCTATCCACTGGCCCTGTGTGT 537
QY 504 GGAGATCAAACTGGTTCTCCGCTGACTCTGGGATCGCTGGTCAAGGGCTACTTCCCTGAG 563
Db 538 GGAGATCAAACTGGTTCTCCGCTGACTCTAGGATGGCTGGTCAAGGGTTATTTCCCTGAG 597
QY 564 TCAGTGACTGTGACTTGAACCTCTGATCCCTGTCCAGCAGTGTGCACACTTCCAGCT 623
Db 598 CCAGTGACCTTGACCTGGAACCTCTGGATCCCTGTCAGTGGTGTGCACACTTCCAGCT 657
QY 624 CTCCTGCACTGTGACTCTACACTATGAGCAGCTCAGTGTCTCCCTCCAGCAGCTGG 683
Db 658 GTCTGCACTGTGACTCTACACCTCAGCAGCTCAGTGTAACTCGAGGACCTGG 717
QY 684 CCAAGTCAGACCTGACCTGGAGGCTGTCCACCCAGCAGCAGCAGCAGCTGACAA 743
Db 718 CCCAGCAGTCCATCACCTGCAATGTGGCCACCCGGAAGCAGCAGCAGCTGACAA 777
QY 744 AAATTTGAGCCCGAGGCGCCATTTCAACAACCTGTCCTCCATGCAAGGAGTGT 803
Db 778 AAATTTGAGCCCGAGGCGCC-----ACAATCAAGCCCTGTCTCTCCATG----- 821
QY 804 CACAAATGCCAGCTCTTAACCTCGAGGGTGGACCATCCGCTCTTCATCTTCCTCCAAAT 863
Db 822 --CAAATGCCAGCAGCCTAACCTCTGGTGGACCATCCGCTCTTCATCTTCCTCCAAAG 879
QY 864 ATCAAGGATGTACTCATGATCTCCCTGACACCCAAAGTCACTGTGTGGTGGTGGATGTG 923
Db 880 ATCAAGGATGTACTCATGATCTCCCTGAGCCCATAGTCAATGTGTGGTGGTGGATGTG 939
QY 924 AGCGAGGATGACCCAGAGCTCCAGATCAGCTGGTTTGTGAACAACCTGGAAGTACACACA 983
Db 940 AGCGAGGATGACCCAGAGTGTCCAGATCAGCTGGTTTGTGAACAACCTGGAAGTACACACA 999
QY 984 GCTCAGACACAAACCCATAGAGAGATTTACAACAGTACTATCCGGGTGTCAGACCCCTC 1043
Db 1000 GCTCAGACACAAACCCATAGAGAGATTTACAACAGTACTCTCCGGGTGTCAGTCCCTC 1059
QY 1044 CCCATCCAGCAGCAGGACTGGATGGTGGCAGGAGTTCAATGCAAGGTCAACAAACAAA 1103
Db 1060 CCCATCCAGCAGCAGGACTGGATGGTGGCAGGAGTTCAATGCAAGGTCAACAAACAAA 1119
QY 1104 GACTCCCATCACCAGTGGAGAGAACCTATCTCAAAAATAAAGGGCTAGTCAGAGCTCCA 1163
Db 1120 GACTCCAGCAGCAGTGGAGAGAACCTATCTCAAAACCCAAAGGCTCAGTAAGAGCTCCA 1179
QY 1164 CAACTATACATCTTGGCCGCCACAGCAGCAGTGTGTCAGGAAAGATGTGCTCAGTCTCACT 1223

[illegible]

RESULT 11

US-09-795-515-6

US-03-733-315 0
: sequence 6. Application US/09795515

sequence 6, Application.
: GENERAL INFORMATION.

GENERAL INFORMATION:
ADDRESSEE: Mr. J. Edgar Hoover

APPLICANT: ADALF, John R.
APPLICANT: Attyal Dilteet S

APPLICANT: Athwal, Diljeet S.

APPLICANT: Entage, John S.

; TITLE OF INVENTION: HUM

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mac

; STREET: One Liberty

CITY: Phi

STATE: PA

COUNTRY: U.S.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM LIFE: floppy disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS

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; . SOFTWARE: PatentIn Release #1.0,
; . CURRENT APPLICATION DATA:
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; CURRENT APPLICATION

APPLICATION NUMBER

;
; FILING DATE: 07/01/2010

CLASSIFICATION:

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/84

FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yatko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEPHONE: (215) 568-3433
TELEFAX: (215) 568-3433

TELEFAX: (213) 368-3439
INFORMATION FOR SEQ ID NO:; INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS

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; LENGTH: 1570 base
TYPE: unaligned

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TYPE: nucleic acid

STRANDEDNESS:

; TOPOLOGY: line

MOLECULE TYPE: CDNA

;; CURRENT APPLICATION NUMBER: US/60/360,207
;; CURRENT FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 47235
;; SEQ ID NO 19352
;; LENGTH: 8600
;; TYPE: DNA
;; ORGANISM: HUMAN
US-09-770-916-1.1.rnrm

Query Match 57.9%; Score 919.8; DB 80; Length 8600;
Best Local Similarity 99.8%; Pred. No. 5.3e-215;
Matches 921; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

540 CTGCTCAAGGCTACTTCCCTGAGTCAGTCTGACTTGGAACTCTGGATCCCTGTCC 599
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4863 CTCTCAAGGCTACTTCCCTGAGTCAGTCTGACTTGGAACTCTGGATCCCTGTCC 4922
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600 AGCAGTGTGCACACTTCCCACTCTCTCGAGCTTGGACTCTACATATGAGCAGCTCA 659
|||
4923 AGCAGTGTGCACACTTCCCACTCTCTCGAGCTTGGACTCTACATATGAGCAGCTCA 4982
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660 GTGACTGTCCCTCCAGCAGCTGGCCAACTGAGCCCTGAGCTGAGAGGTTGCTCACCCA 719
|||
4983 GTGACTGTCCCTCCAGCAGCTGGCCAACTGAGCCCTGAGCTGAGAGGTTGCTCACCCA 5042
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720 GCCAGCAGCACCAGGTTGACAAAACCTTGAGCCCGAGCGGCCCATTTCAACATCAAC 779
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5043 GCCAGCAGCACCAGGTTGACAAAACCTTGAGCCCGAGCGGCCCATTTCAACATCAAC 5102
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780 CCCTGTCTCTCCATCAAGGAGTGTACAAATGCCAGCTCTTAACCTCGAGGTTGAGCA 839
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5103 CCCTGTCTCTCCATCAAGGAGTGTACAAATGCCAGCTCTTAACCTCGAGGTTGAGCA 5162
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840 TCCGTCTTCTCTCCCTTCAAAATATCAAGGATGTATCATGATCTCCCTGACACCCCAAG 899
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5163 TCCGTCTTCTCTCTCCCTTCAAAATATCAAGGATGTATCATGATCTCCCTGACACCCCAAG 5222
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900 GTGACGTGTGTGGTGGTGTGAGTGTGAGGAGATGATCCAGAGCTCCAGATCAGTGGTTT 959
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5223 GTGACGTGTGTGGTGGTGTGAGTGTGAGGAGATGATCCAGAGCTCCAGATCAGTGGTTT 5282
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960 GTGAACACAGTGGAGTGTACACACAGCTCAGACAAACCCATAGAGAGGATTAACAAGT 1019
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5283 GTGAACACAGTGGAGTGTACACACAGCTCAGACAAACCCATAGAGAGGATTAACAAGT 5342
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1020 ACTATCCGGTGTGTGACACCCCTCCCATCCAGCAGGAGTGTGATGAGTGGCAAGGAG 1079
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1080 TTCAATGCAAGTGTACAAACAAAGACCTCCCATCCAGCAGGAGTGTGATGAGTGGCAAG 1139
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1140 ATTAAGGGCTAGTTCAGAGCTCCCAAGTATACATCTTGGCCGCCACAGCAGGAGTTG 1199
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5463 ATTAAGGGCTAGTTCAGAGCTCCCAAGTATACATCTTGGCCGCCACAGCAGGAGTTG 5522
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1200 TCCAGGAAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1259
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5523 TCCAGGAAGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 5582
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1260 GTGAGTGGACAGCAATGGGATACAGAGGAGAACTACAGAGCAGCAGCAGCAGCAGCAGT 1319
|||
5583 GTGAGTGGACAGCAATGGGATACAGAGGAGAACTACAGAGCAGCAGCAGCAGCAGCAGT 5642
|||
1320 GACTCTGACGGTCTTACTTCAATATAGCAAGTCAATATGAAACAAAGCAAGTGGGAG 1379
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5643 GACTCTGACGGTCTTACTTCAATATAGCAAGTCAATATGAAACAAAGCAAGTGGGAG 5702
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1380 AAAACAGATCTCTTCTATGCAACGTGAGACACAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 1439
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5703 AAAACAGATCTCTTCTATGCAACGTGAGACACAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 5762
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QY 1440 AAGACCATCTCCCGGTCTCCGGG 1462
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Db 5763 AAGACCATCTCCCGGTCTCCGGG 5785

RESULT 14
US-07-688-197-2
; Sequence 2, Application US/07688197
; GENERAL INFORMATION:
; APPLICANT: FOUSSER, LYNETTE A
; APPLICANT: SWANBERG, STEPHEN L
; TITLE OF INVENTION: RECOMBINANT 3F8-TYPE ANTIBODIES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC. - LEGAL AFFAIRS
; ADDRESS: DEPARTMENT
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,197
; FILING DATE: 19910419
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCDANIELS, PATRICIA A
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: GI 5168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 876-1170 EXT. 405
; TELEFAX: 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1462 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; CELL TYPE: Hybridoma
; CELL LINE: 957
; IMMEDIATE SOURCE:
; CLONE: P3F8GAMMA3.21
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..4
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1412..1462
US-07-688-197-2

Query Match 56.7%; Score 900; DB 3; Length 1462;
Best Local Similarity 77.2%; Pred. No. 2.1e-210;
Matches 1133; Conservative 0; Mismatches 305; Indels 30; Gaps 2;

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QY 89 CCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 148
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Db 61 CCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 120
|||
QY 149 CACCTGGACAGTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 208
|||

121 CACTTGCACCTCTCTGGGTTTTCAGTAACCAATATATGGTGTACACTGGGTTCGCCAGCC 180
209 TCCAGGAAAGGCTCGAGTGGCTGGAGTATATGGAGTGGTGGAGACACAGACTATAA 268
181 TCCAGGAAAGGCTCGAGTGGCTGGAGTATATGGGCTGGTGAATACAAATATAA 240
269 TGCAGCTTTTCATATCCAGACTGACATCAGCAAGGACAAATTCGAAGAGCCAACTCTCT 328
241 TTCCGCTTTTCATATCCAGACTGACATCAGCAAGGACAAATTCGAAGAGTCAAGTTTCT 300
329 TAAATGAACAGCTCGGAGTACTGACACAGCCATATATCTGTGCGCAAAATAGAGG 388
301 AAAATGAACAGCTCGAAATGTATGACACAGCCATGACTGTGCGCAAGTGGGGGGG 360
389 GGATATTTACTATGATTTCACTTATGCTTATGCTGAGTGGGCTCAAGGAACCTCAGTCAC 448
361 -----TCACTACGGCTATGCTTTGGACTACTGGGCTCAAGGAACCTCAGTCAC 408
449 CGTCTCTCAGCAAAACACACCCCATCATCTATCCACTGGCCCTGGGTGGGAGA 508
409 CGTCTCTCAGCTACCAACACAGCCCATCTGTCTATCCCTGGTCCCTGGCTGCACTGA 468
509 TACAACCTGTTCCCTCGGACTCTGGATGCTGGTCAAGGGCTACTTCCCTGGAGTCACT 568
469 CACATCTGGATCTCGGTGACACTGGGATGCTTGTCAAAGGCTACTTCCCTGGAGCCGGT 528
569 GACTGTGACTTGGAACTCTGGATCTGCTGACAGCTGTGACACACCTTCCAGCTCTCT 628
529 AACTGTAAATGGAATATGAGCCCTTCCAGCCGCTGTGCGCACAGTCTCTATCTGTCT 588
629 GCAGTCTGGACTACACTATACAGCTGCTGACTGTCTCCCTCCAGCAGCTGSCCAAG 688
589 GCAGTCTGGTCTATCTCCCTCAGCAGCTGTGACTGTACCTCCAGCAGCTGSCCCAG 648
689 TCAGACCTGACCTGACGCTGTCTACCCAGCCAGCAGCAGCAGCTGGAGCAAAAACT 748
649 CCAGACTGTCTGCTGACAGCTAGCCACCCAGCAGCAGCAGCTGAGTTGATCAAGAGAT 708
749 TGAGCCACGCGGCCATTTCAACAATCAACCCCTCTCTCCATGCAAGAGAGTGTCAAA 808
709 CGAGCTAGATACCAAGCCAGTACCCCCAGCTTCTC----- 750
809 ATGCCAGCTCTTAACCTGAGGCTGGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 868
751 ATGCCAGCTCTTAACCTGAGGCTGGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 810
869 GGATCTACTGATCTCTCTGACACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 928
811 GGATCTACTGATCTCTCTTAACCCCAAGCTTACGTTGCTGCTGCTGCTGCTGCTGCTG 870
929 GGATCTACTGATCTCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
871 GGATCTACTGATCTCTCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
989 GACACAAACCATAGAGAGGATTAACAGTACTATCCGGGTGGTGGTGGTGGTGGTGGTGG 1048
931 GACACAGCCGCTGAGAGTCTGATTAACAGTACTATCCGGGTGGTGGTGGTGGTGGTGGT 990
1049 CCAGCAGGAGTGGATGAGTGGAGGATTAACAGTACTATCCGGGTGGTGGTGGTGGTGGT 1108
991 CCAGCAGGAGTGGATGAGTGGAGGATTAACAGTACTATCCGGGTGGTGGTGGTGGTGGT 1050
1109 CCCATCCCATCGAGAGAACCATCTCAAAATTAAGGGCTAGTCAGAGCTTCCCAAGT 1168
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1169 ATACATCTTGGCCGACAGAGAGTGTGTCAGAGAAAGATGTCAGTCTCTCTCTCTCTCT 1228
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1229 GGTCTGGGCTTCAACCCCTGGAGATCAGTGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1288

1171 GGTCAACCACTTCTCTGAAGCCATCAGTGTGGAGTGGGAAAGGAGGAGAACTGGA 1230
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1231 CGAGATTACAAGAACACTCCACCCATCTGAGCTAGATGGAGCTACTTCTCTCTACAG 1290
1349 CAAGCTCAATATGAACCAAGCAAGTGGAGAAACAGATTCCTTCTCATGCAAGCTGAG 1408
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1409 ACAGAGGCTCTGAAAATTTACTACTGAAGAGACCATCTCCCGTCTCCGGGTAAATG 1468
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1411 AGACAGCACCTAGCCATCTCCTCGGTC 1438

RESULT 15
US-09-629-430B-3
; Sequence 3, Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
; TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7528
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; cDNA
US-09-629-430B-3

Query Match 55.7%; Score 885; DB 24; Length 7528;
Best Local Similarity 77.8%; Pred. No. 1.9e-206;
Matches 1116; Conservative 0; Mismatches 295; Indels 24; Gaps 3;

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DB 1246 CTTGTGTTCTTCTCTCTCTGCTGGTGCAGCTCCAGATGGGTCCTGTCCTCCAGGTCAGCT 1305
QY 101 GAAGCAGTCAGGACCTGGCTAGTGCAGCCCTCAGAGCCTGTCCATCACCCTGCACAGT 160
DB 1306 ACAGCAGTGGGCGCAGGACTGTTGAAGCTTCGAGACCTGTCCTCACCCTGCGGTGT 1365
QY 161 CTCTGCTTCTCATTAACCTAGCTATGGTGTACACTGGTGTGCTGCTAGTCTCTCCAGGAAAGG 220
DB 1366 TTATGGTGGTCTCTCAGTGGTGTACTGAGGCTGTGATCCGCCAGCCCGGAGGAGG 1425
QY 221 TCTGGAGTGGCTGGGAGTGTATGGAGTGGTGGAGACACAGACTATAATGACGCTTTCAT 280
DB 1426 GCTGGAGTGGATGGGAAATCAATCATAGTGAAGACCACTACAACCCCTCCCTCAA 1485
QY 281 ATCCAGCTGAGCATCAGCAAGGACAAATTCAGAGGCACTCTCTTTTAAATGAACAG 340
DB 1486 GAGTCCGAGTCACTATCATGACACAGCTGCCAAGAGCAGCTCTCTCCCTGAGTGTAGCTC 1545
QY 341 TCTGGAGCTACTGACAGCCATATATCTAGTGTCCAGA-----AATAGAGGGATAT 394
DB 1546 TGTGAACCCGCGGACACGGCTGTGTATCTACTGCGAGAGTTATCTAGTGGCGGAGTCC 1605
QY 395 TTACTATGATTTTCACTTATGCTATGCTAGTGTGGTGTCAAGGAACTCAGTCACTGCTC 454
DB 1606 TGGCAGACAGGGAGGTACGGTATGACCTCTGGGCGCAAGGACCCAGCTCAGGCTC 1665

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455 CTCAGCCAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGGAGATACAAC 514
1666 CTCGGCCAAACGGCCCGCCATCGGTCTATCCACTGGCCCTGGGTGGAGATACAAG 1725
515 TGGTTCCTCCGTGACTCTGGGATGCTCAAGGGCTACTTCCCTGAGTCACTGCTGT 574
1726 TGGCTCCTCGGTGACTCTAGGATGCTGTCAAGGGTATTTCCCTGAGCCAGTCACTT 1785
575 GACTTGGAACTCTGGATCCCTCTCCAGCAGTGTGACACACTTCCCACTCTCTCTGAGTC 634
1786 GACCTGGAACCTCTGGATCCCTCTCCAGTGTGTGACACACTTCCCACTCTCTCTGAGTC 1845
635 TGGACTCTACACTATGAGCAGCTCAGTCACTGCTCCCTCCAGCAGTGTGAGCAGAC 694
1846 TGACCTCTACACCTCAGCAGCTCAGTCACTGCTTAACCTGAGCAGTGTGAGCAGCAGTC 1905
695 CCTCAGCTCAGCTGTGTCACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 754
1906 CATTACCTGCAATGTGGCCCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1965
755 CAGCGGGCCCATTTCAACAATCAACCCCTGTCTCCATGCAAGGAGTGTACACAAATGCC 814
1966 CAGAGGGCCC-----CAATCAAGCCCTGTCTCCATG-----CAATGCC 2007
815 AGCTCCTAACCTCAGGAGGAGCCTCCGCTTTCATCTTCCCTCCAAATATCAAGGATGT 874
2008 AGCACCTAACCTCTTGGGTGGACCTCCGCTTTCATCTTCCCTCCAAAGATCAAGGATGT 2067
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2128 CCAGATGCTCCAGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2187
995 AACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAACAGCTCCCTCCCTCCAGCA 1054
2188 AACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAACAGCTCCCTCCCTCCAGCA 2247
1055 CCAGGAGTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCCTCCATC 1114
2248 CCAGGAGTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCCTCCAGC 2307
1115 ACCCATCGAGAGAACCATCTCAAAATTAAGGGCTAGTCAAGCTCCCAAGTATACAT 1174
2308 GCCCATCGAGAGAACCATCTCAAAATTAAGGGCTAGTCAAGCTCCCAAGTATATGT 2367
1175 CTTGCCGCCACGACGAGCAGTGTGCTCCAGGAAGATGCTCAGTCTCAGTCTCAGTCTGCTG 1234
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2548 GAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCTCTGTTGCTGCTGCTGCTG 2607
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GenCore version 5.1.6
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MM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 22:24:31 ; Search time 257.965 Seconds
(without alignments)
9033.299 Million cell updates/sec

Title: US-09-770-916-1

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Sequence: 1 ccatctctctcatagc.....taaaaaaaaaaaaaaaaaaa 1588

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 segs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance; to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	939.2	59.1	1570	9	US-09-795-515-6
2	740.8	46.6	1676	10	US-09-815-837-82
3	684.8	43.1	2053	10	US-09-815-837-63
4	684.8	43.1	2059	10	US-09-815-837-66
5	662	41.7	1516	9	US-09-903-327A-1
6	654.6	41.2	1798	9	US-09-925-299-230
7	654.6	41.2	1798	10	US-09-925-299-230
8	648.8	40.9	1392	9	US-10-216-484-8
9	638.8	40.2	1413	9	US-10-153-382-16
10	636.6	40.1	1708	10	US-09-859-053-31
11	635	40.0	1673	10	US-09-859-053-35
12	634.6	40.0	1428	10	US-09-740-002-17
13	630.8	39.7	1431	9	US-10-124-905-11
14	630.8	39.7	1431	9	US-09-948-429B-11
15	629.2	39.6	1431	9	US-10-073-138-6
16	626.6	39.5	1428	10	US-09-740-002-19
17	620.6	39.1	1392	9	US-10-150-475A-7
18	620.2	39.1	4191	9	US-10-176-380-18
19	618.4	38.9	8120	9	US-09-736-258-68

20	618.2	38.9	1449	10	US-09-747-669-1
21	618.2	38.9	1449	10	US-09-747-669-2
22	618	38.9	1431	9	US-10-124-905-3
23	618	38.9	1431	9	US-09-948-429B-3
24	617	38.9	1392	9	US-10-153-382-12
25	616.8	38.8	1404	9	US-10-211-357-9
26	616.8	38.8	1404	9	US-10-211-357-11
27	616.8	38.8	1565	10	US-09-822-849A-104
28	616.4	38.8	1431	9	US-10-073-138-2
29	615.2	38.7	1404	9	US-10-211-357-7
30	615	38.7	1395	9	US-10-153-382-8
31	613.4	38.6	1420	10	US-09-237-061-2
32	612.2	38.6	1392	9	US-10-153-382-1
33	609.6	38.4	1539	10	US-09-822-849A-87
34	609	38.4	1392	9	US-10-153-382-4
35	608.4	38.3	1356	10	US-09-822-698A-27
36	607.6	38.3	1605	10	US-09-822-830A-501
37	607.6	38.3	1617	10	US-09-822-830A-571
38	606.8	38.2	1616	10	US-09-859-053-27
39	605	38.1	1599	10	US-09-954-456-789
40	605	38.1	1599	10	US-09-954-456-1604
41	605	38.1	1616	10	US-09-822-830A-572
42	603.8	38.0	3300	9	US-10-020-786-2
43	603.6	38.0	1347	10	US-09-736-371B-20
44	602.6	37.9	1427	12	US-10-066-895-20
45	602.6	37.9	1427	12	US-10-066-895-25

ALIGNMENTS

RESULT 1

US-09-795-515-6
; Sequence 6, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yattoo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1570 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; ,
LENGTH: 16/6

; ,
LENGTH: 16/6

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; TYPE: DNA
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pcB223
; OTHER INFORMATION: recombinant MHC class II heterodimer
US-09-815-837-82

Query Match 46.6%; Score 740.8; DB 10; Length 1676;
Best Local Similarity 84.7%; Pred. No. 6.8e-219;
Matches 861; Conservative 0; Mismatches 137; Indels 18; Gaps 2;

456 TCAGCCAAACACACCCCATCAGTCTATCCAGTGGCCCTGGGTGGAGATACAACT 515
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673 TCTGCCAAACACACCCCATCAGTCTATCCAGTGGCCCTGGGTGGAGATACAACT 732
   |||||
516 GTTCTCTCGTACGCTGGAGTGGTCAAGGGTACTTCCCTGAGTCAAGTGTGG 575
   |||||
733 GGCTCTCGTACGCTGGAGTGGTCAAGGGTATTTCCCTGAGCAGTCAAGCTTG 792
   |||||
576 ACTTGGAACTCTGGATCCCTGCCAGCAGTGGACACCTTCCAGCTCTCCAGCTG 635
   |||||
793 AGCTGGAACCTCTGGATCCCTGCCAGTGGTGGACACCTTCCAGCTCTCCAGCTG 852
   |||||
636 GGACTCTACACTATGAGCAGCTGAGTCTGCCCTCCAGCAGCTGGCCAAAGTCAG 695
   |||||
853 GACCTCTACACCTCAGCAGCTGAGTCTGAACTCCGAGCAGCTGGCCCAAGCTCC 912
   |||||
696 GTCACTCAGCGTTGTCACCCAGCAGCAGCAGCAGTGGGCAAAACCTTGAGCC 755
   |||||
913 ATCACTGCAATGTGCCCAACCCGCGAGCAGCAGCAGTGGGCAAAACCTTGAGCC 972
   |||||
756 AGCGGGCCATTTCAACAAATCAACCCCTGTCCTCATGCAAGGAGTGTCAAAATG 815
   |||||
973 AGAGGGCC-----ACAATCAAGCCCTGCTCTCATG-----CAATGCCCA 1014
   |||||
816 GCTCTTAACCTCAGGCTGGACCACTCCGCTCTTCATCTCCCTCCAAATATCAAG 875
   |||||
1015 GCACCTAACCTCTTGGGTGGACCACTCCGCTCTTCATCTCCCTCCAAAGATCAAG 1074
   |||||
876 CTCATGATCTCCCTGACACCCCAAGTCACTGCTGTGGTGGTGGAGTGTGAGCG 935
   |||||
1075 CTCATGATCTCCCTGAGCCCAATGATGATGCTGTGGTGGTGGTGGAGTGTGAGCG 1134
   |||||
936 CCAGAGCTCCAGATCAGCTGTTTGTGAACACAGTGGAGTACACACAGCTCAGAC 995
   |||||
1135 CCAGATGTCAGATCAGCTGTTTGTGAACACAGTGGAGTACACACAGCTCAGAC 1194
   |||||
996 ACCCATAGAGAGGATTAACACAGTACTATCCGGGTGGTCAAGCAGCTCCCATC 1055
   |||||
1195 ACCCATAGAGAGGATTAACACAGTACTATCCGGGTGGTCAAGCAGCTCCCATC 1254
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1056 CAGGACTGGATGAGTGGCAAGGATTAACATCAAGTTCACACAAAGACCTCCCAT 1115
   |||||
1255 CAGGACTGGATGAGTGGCAAGGATTAACATCAAGTTCACACAAAGACCTCCCAT 1314
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1116 CCATCAGAGAACCATCTCAAAATTAAGAGGCTAGTCAAGCTCCACAAAGATATAC 1175
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1315 CCATCAGAGAACCATCTCAAAATTAAGAGGCTAGTCAAGCTCCACAGGATATG 1374
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1176 TTGCGCCACCCAGCAGAGCAGTGTTCAGAGAAAGATGTCACTTCCCTGCTGCTG 1235
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1375 TTGCTCCACCCAGAGAGAGATGACTAAGAACAGGCTCACTTCACTGCTGCTGCT 1434
   |||||
1236 GGCTTCAACCTCGGAGACATCAGTGTGAGTGGACCAAGTTCAGGATATACAGGAG 1295
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1435 GACTTCATGCTGAAGACATTTACGTGGTGGACCAACAGCGGAAACAGAGCTAAAC 1494
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1296 TACAGGACACCGCAGCAGTCTGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1355
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1495 TACAGGACACTGACAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1554
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1356 AATATGAACACAGCAAGTGGGAGAAACAGATCTTCTCATGCAACGTGAGACAG 1415
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RESULT 3

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US-09-815-837-63
; Sequence 63, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 2053
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 90-101
; OTHER INFORMATION: CH1.H.2 recombinant MHC class II-peptide-Ig
; OTHER INFORMATION: fusion complex
US-09-815-837-63
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Query Match 43.1%; Score 684.8; DB 10; Length 2053;
Best Local Similarity 99.7%; Pred. No. 1.7e-201;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

458 AGCCAAACACACCCCATCAGTCTATCCAGTGGCCCTGGGTGGAGATACAACTGG 517
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1353 AGCCAAACACACCCCATCAGTCTATCCAGTGGCCCTGGGTGGAGATACAACTGG 1412
   |||||
518 TTCCCTCCGCTGACTCTGGGATGCTGTCAAGGCTACTTCCCTGAGTCACTGTGAC 577
   |||||
1413 TTCCCTCCGCTGACTCTGGGATGCTGTCAAGGCTACTTCCCTGAGTCACTGTGAC 1472
   |||||
578 TTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACTTCCAGCTCTCCAGTCTGG 637
   |||||
1473 TTGGAACTCTGGTCCCTGTCCAGCAGTGTGCACACTTCCAGCTCTCCAGTCTGG 1532
   |||||
638 ACTCTACACTATGACAGCTCAGTCTGCTCCCTCCAGCAGCTGGCCAAAGTCAAG 697
   |||||
1533 ACTCTACACTATGACAGCTCAGTCTGCTCCCTCCAGCAGCTGGCCAAAGTCAAG 1592
   |||||
698 CACTGTCAGCTGTGCTACCCAGCAGCAGCAGCGTGGACAAAACCTTGAGCCAG 757
   |||||
1593 CACTGTCAGCTGTGCTACCCAGCAGCAGCAGCGTGGACAAAACCTTGAGCCAG 1652
   |||||
758 CGGGCCCATTTCAACAAATCAACCCCTGTCTCCATGCAAGGAGTGTCAAAATGCC 817
   |||||
1653 CGGGCCCATTTCAACAAATCAACCCCTGTCTCCATGCAAGGAGTGTCAAAATGCC 1712
   |||||
818 TCCTAACCTCGAGGGTGGACCATCCGTCTTCACTTCCCTCCAAATATCAAGATG 877
   |||||
1713 TCCTAACCTCGAGGGTGGACCATCCGTCTTCACTTCCCTCCAAATATCAAGATG 1772
   |||||
878 CATGATCTCCCTGACACCCAGCAGCTGTGCTGGTGGATGTGAGCAGGATGACCC 937
   |||||
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196 GGGTTGCTCAGTCTCCAGGAAGGGTCTGGAGTGCGCTGGAGATGATATGGAGT---GGTG 252
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

191 GGGTCAGACAGAGCCATGGAAAGAGCGCTTGAGTGGATTGGATATATTTTATCCTTACAAG 250
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

253 GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGACAGCAATTTCCA 312
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

251 GTGTACTGGCTTAACCCAGAAGTTCAAGAGCACAGGCCACATGTGACACACAGCAAGTTCCCT 310
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

313 AGAGCCAACTCTTCTTTAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACT 372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

311 CCAACACAGCTACATGGAGCTCCGAGCGCTGACATCTGATGCCCTGCACTCTATTACT 370
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

373 GTGCCAAGAAATAGAGGGGATATTACTATGATTTCACTTATGCCATGACTACTGGGGTC 432
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

371 GTGCAAGA-----GGGATTCTTACTGGGGCC 397
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

433 AAGAACTCAGTCACGCTCTCTCCTCAGCCAAAACACCACCCCATCAGTCTATCCATCG 492
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

398 AAGGGACTCTGGTCACTGTCTCTGACGCCAAAACACACACCCCATCTGCTATCCATCG 457
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

493 CCCCTGGGTGGAGATACAACTGGGTTCCTCCGTGACATCTGGGATGCTGCTCAAGGGCT 552
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

458 CCCCTGGATCTGTGCCAAACTAACTCCATGGTGACCTGGGATGCTGGTCAAGGGCT 517
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

553 ACTTCCCCTGAGTCAGTGTGACTGTGACTTTGAACTCTGGATCCTCTGCCAGCAGTGTGCACA 612
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

518 ATTTCCCCTGAGCCAGTGACAGTGACCTGNACTCTGGATCCTGTCCAGCGGTGTGCACA 577
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

613 CCTTCCCAGCTCTCCTGCAGCTGGACTCTACACTATCAGCAGCTCAGTGACTGTCCCT 672
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

578 CCTTCCCAGCTCTCCTGCAGCTGTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCT 637
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

673 CCAGCAGCTGGCCAAAGTCAGACCGTCACTCGAGCGTTGCTTCAACCAGCCAGCAGCACCA 732
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

638 CCAGCAGCTGGCCACCGAGACCGTCACTCGAACGTTGCCACCCCGCCAGCAGCACCA 697
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

733 CGGTGGCAAAAAACTTTGAGCCACGCGGGSCCATTTCAAACAATCAACCCCTGTCTCCAT 792
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

698 AGGTGGACAAGAAATGTGCCAGGATTGTGGTTGTAAAGCTTGCATATG----- 749
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

793 GCAAGGAGTGTCAAAATGCCAGCTCTTAACCTCGAGGGTGGACCATCCGCTTTCATCT 852
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

750 -----TACAGTCCCAGAGTATCATCTGTCTTCACT 761
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

853 TCCTTCCAAATATCAAGGATGTA CTATGATCTCCTGACACCCAAAGTCACTGTGTGG 912
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

782 TCCCCCAAGCCCAAGGATGTCTCACATTACTCTGACTCTCTAAAGTCACGTGTGTG 841
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

913 TGGTGATGTGACGAGGATGATCCAGAGCTCCAGATCAGCTGTTGTGTGAACAAAGTGG 972
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

842 TGTGATGACATCAAGAGGATGATCCGAGGTCCAGTTCAGCTGTTGTAGATGATGTGG 901
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

973 AAGTCACACAGCTCAGACACAAAACCCATAGAGGATTACACAGTACTATTCGGGTGG 1032
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

902 AGGTGGACACAGCTCAGACGCACACCCGAGGAGCAGTTCACAGCAGCTTTCGCTCAG 961
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1033 TCAGCACCTTCCCATPCCAGCACACAGGACTGGATGAGTGGCAAGSAGTTCAAATGAAG 1092
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

962 TCAGTGAATTCCTCATGACACAGGACTGGCTCAATGGCAAGGATTCAAATGACAGG 1021
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1093 TCACACAAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAATTTAAAGGGCTAG 1152
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1022 TCAACAGTCAGCTTTCCTTGCCTCATCGAANAACCATCTCAAAACCAAGGCAGAC 1081
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1153 TCAGAGCTCCAAGATATACATCTTTGCGCCACCAAGCAGCAGTGTCTCCAGGAAGATG 1212
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

1082 CGAAGGCTCCACAGGTGTACACCATTCACCTCCCAAGGACAGATGGCCAAAGATAAG 1141
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1213 TCAGTCTCACTTGCCTGGCTGTGGGCTTCAACCTGGAGACATCAAGTGTGGATGGACCA 1272
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

142 TCAGTCTGACCTGCATGATTAACAGACTTCTTCCCTGAAGACATTACTGTGCAAGTGCAGT 1201
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

	Qy	1273	GCAATGGGCATTACAGGAGAGAACTACAAGGACACCGCCACCTCCTGGACTCTGTGCGTTT	1333
	Dd	1202	GAATGGCCAGCCAGCGGAGAACTACAAGAACACTCACGCCCATCATGGACACAGATGGCT	1261
	Qy	1333	CCTACTTCATATATAGCAGCTCAAATATGAAAACAAGCAAGTGCGGGAAAAA CAGATTCCT	1392
	Dd	1262	CCTACTTCGCTCFACAGCAGCTCAAATGTGCAAGAGCAACTGGGAGCGCGGAAATACTT	1321
	Qy	1393	TCTCATGCAACTGAGACACGAGGGCTCTCAAAATTA CTACCTGAAGAGACATCTCCC	1452
	Dd	1322	TCATCTGCTCTGTGTACATGAGGCGCTGCACAACCCAT ACTGAGA GAGCCTCTCCC	1381
	Qy	1453	GGTCFCGGGTAAATTAGCTCAGCAGCACCAAGCTCTCAGGTCTCTAAGAGACACTGGCA	1512
	Dd	1382	ACTCTCTCGTAAATGATCCCCAGTGTCTTGAGGCCCTCTGGTCTCTACAGSACTCTGTCA	1441
	Qy	1513	CCCATATCCATGCATCCCTTGTTATAATAAAGCATCCAGCAAGCCTGGTACCATGTAAA	1572
	Dd	1442	CCTACTCCACCCCTCCC-TGTATATAATAAGCACCTAGCACTGCTTGGGAGCCCTGCA A	1500
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	Dd	1501	TAAAAAAAAAAAAAAAAA 1516	

RESULT 6

US-09-925-299-230	Sequence 230, Application US/09925299
Publication No. US20030040617A9	
GENERAL INFORMATION:	
APPLICANT: Rosen et al.	
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies	
FILE REFERENCE: PA102	
CURRENT APPLICATION NUMBER: US/09/925,299	
CURRENT FILING DATE: 2001-08-10	
PRIOR APPLICATION NUMBER: PCT/US00/05883	
PRIOR FILING DATE: 2000-03-08	
PRIOR APPLICATION NUMBER: 60/124,270	
PRIOR FILING DATE: 1999-03-12	
NUMBER OF SEQ ID NOS: 1556	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 230	
LENGTH: 1798	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: (1)	
OTHER INFORMATION: n equals a,t,g, or c	
NAME/KEY: misc_feature	
LOCATION: (15)	
OTHER INFORMATION: n equals a,t,g, or c	
NAME/KEY: misc_feature	
LOCATION: (24)	
OTHER INFORMATION: n equals a,t,g, or c	
NAME/KEY: misc_feature	
LOCATION: (31)	
OTHER INFORMATION: n equals a,t,g, or c	
NAME/KEY: misc_feature	
LOCATION: (501)	
OTHER INFORMATION: n equals a,t,g, or c	
NAME/KEY: misc_feature	
LOCATION: (1798)	
OTHER INFORMATION: n equals a,t,g, or c	
US-09-925-299-230	

	Query Match	41.2%	Score	654.6	DB	9	Length	1798
	Best Local Similarity	66.3%	Pred.	No.	3.7e-192			
	Matches	1013	Conservative	10	Mismatches	475	Indels	30
								Gaps
								5
55	TCTGCTGGTGACATTC	CCCAAGCTGTGCTCTATCC	CAGGTGCAGCTGCAGCTGCAGGAC	CTCAGGAC	114			
170	TTTTCCTCGTGTCTCT	TTTAAAGAGTGTCCAGTGT	CAGCTGTGAGCTGGTGGAGCTCTGGGG	229				

20 TCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTCTCAGGTCCAACTGCAGCAGCGCTG 79

112 GACCTGGGCTAGTGCAGCCCTCACAGAGCGTGTCCACTCACCTGCAGACGTCTCTGTTTCT 171

80 GGGCTGAGCTTGTGAAAGCGCTGGGGCTTCAGTGAAGCTGTCTGTGCAAGGCTTCTGGCTACA 139

172 CATTAACTAGCTATGTTGTATACACTGGGTTGTCAGTCTCCAGGAAAGGGTCTGGAGTGC 231

140 CCTTCACCAGCTACTGGATGCAGTGGGTAAACAGAGGCCGTGCACAGGCGCTTCAGTGGGA 199

232 TGGGAGTGTATGATGAGTGTGGGAGACACAGACTATTAATGCAGCTTTTCATATCCAGAC 288

200 TCGGAGAGATTGATCTCTTCATAGCTATATACTACTACAAATCAAAAGTTCAAGGCAAGG 259

289 TGAGCATCAGCAACGACAAATTCGAAGGCCAACTCTTCTTTAAATGAACAGTCTGCGAG 348

260 CCACATTTGACTGTATAGACACATCTCCAGCAGACGCTTACATGCAGCTCAGCAGCGCTGACAT 319

349 CTACTGACACAGCCATATATTACTGTGCAGAAATAGAGGGGATATTTACTATGATTTC 408

320 CTGAGGACTCTGGGCTCTATTACTGTGCAAGAAATAGG- - - - -ACTATAGTAACA 370

409 CTTATGCCATGGACTACTCTGGGCTCAGGAACTTCAGTCAACCTCTCTCTCAGCCAAAACAA 468

371 ACTGGTACTTTCATGTCCTGGGGCACAGGGACACAGGTTCACCGTCTCTCAGCCAAAACGA 430

469 CACCCCATCAGTCTATCCACTGGCCCCCTGGGTGGAGATACAACTGGTTTCTCCGTGA 528

431 CACCCCATCTGTCTATCCACTGGCCCCCTGGATCTGCTGCCAAACTAACTCCATGTTGA 490

529 CTCCTGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCACTGACTGTGACTTTGGAACCTCTG 588

491 CCTCTGGGATGCTGGTCAAGGGCTATTTCCTGAGCAGTGCAGTGCAGTCTGGAACTCTG 550

589 GATCCTCTGCAGCAGTGTGCACACCTTCCAGCTCTCCTGCAGTCTGGACTCTACACTA 648

551 GATCCTCTGCAGCGGTGTGCACACCTTCCAGCTCTCCTGCAGTCTCACTCTACACTC 610

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611 TGAGCAGCTCAGTGACTGTCCCTCCAGCACCTTGGCCCAAGTGCAGCAGCGTCACTTCGACG 670

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RESULT 9

REF ID: A66011
US-10-153-382-16

US-10-133-382-16 : Sequence 16 Application US/101533382

; Sequence 16, Application US/101

; Publication No. US20

; GENERAL INFORMATION:

APPLICANT: PFIZER PRODUCTS INC.

; TITLE OF INVENTION: USES

FILE REFERENCE: PC23019A

FILE REFERENCE: FC23013H
CURRENT APPLICATION NUMBER: US/

; CURRENT APPLICATION NUMBER: US/10/1
 : CURRENT FILING DATE: 2002-05-22

; CURRENT FILING DATE: 2002-05
 ; PATENT REGISTRATION NUMBER: 507

; PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 2001-05-

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Pat

: SOE ID NO. 16

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; SEQ ID NO 16
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; LENGTH: 1413

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; LENGTH: 1413
TYPE: DNA

40 28: score 638 8: DB 9: Length 1413:

Query Match

Best Local Similarity 68.5%; Pred. No. 2.6e-187;

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1582 ATACTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1612

; Sequence 35, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: 5'UTR
; LOCATION: (1)...(95)
; NAME/KEY: CDS
; LOCATION: (96)...(1505)
; NAME/KEY: 3'UTR
; LOCATION: (1509)...(1673)
; NAME/KEY: sig_peptide
; LOCATION: (96)...(152)
; US-09-859-053-35

Query Match 40.0%; Score 635; DB 10; Length 1673;

Best Local Similarity 66.2%; Pred. No. 4.3e-186;
Matches 1013; Conservative 0; Mismatches 475; Indels 43; Gaps 5;

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Db 178 GAGGCTTGTACAGCTGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGAATTCACCT 237
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Db 538 AGGGCCCTCTTCCCTCTGGGCCCTGCTCCAGGAGCACTCCGAGAGCAGCAGCG 597
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Db 598 CCCTGGGCTGCTGTGCAAGGACTACTTCCCGAACCCTGACCGGTGCTGCGAACTCAG 657

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:18:11 ; Search time 84.1325 seconds
(without alignments)
5788.524 Million cell updates/sec

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	674.4	42.5	1347	6	5455030-2
5	651.8	41.0	1567	3	US-09-049-672A-17
6	651.2	41.0	1418	4	US-08-793-450-7
7	637.4	40.1	1418	1	US-08-467-420A-49
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13	634.6	40.0	1428	1	US-08-488-376-17
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21	630.8	39.7	1431	3	US-08-487-550-11
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29	626.6	39.5	1428	4	US-09-335-697B-19	Sequence 19, Appl
30	626.6	39.5	1428	4	US-09-335-697B-19	Sequence 19, Appl
31	625.6	39.4	1797	1	US-08-442-542-17	Sequence 17, Appl
32	625.6	39.4	1797	3	US-08-765-469-17	Sequence 17, Appl
33	618.4	38.9	8120	3	US-09-027-449-68	Sequence 68, Appl
34	618.4	38.9	8120	3	US-09-026-985-68	Sequence 68, Appl
35	618.4	38.9	8120	4	US-09-121-952A-68	Sequence 68, Appl
36	618.4	38.9	8120	4	US-09-234-340A-68	Sequence 68, Appl
37	618	38.9	1431	3	US-08-487-550-3	Sequence 3, Appl
38	616.8	38.8	1404	3	US-08-523-894-9	Sequence 9, Appl
39	616.8	38.8	1404	3	US-08-523-894-11	Sequence 11, Appl
40	615.2	38.7	1404	3	US-08-523-894-7	Sequence 7, Appl
41	612.4	38.6	6557	1	US-08-286-740-3	Sequence 3, Appl
42	612.4	38.6	6557	5	PCT-US95-09576-3	Sequence 3, Appl
43	612.2	38.6	1350	1	US-08-157-101A-9	Sequence 9, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 6, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Achwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1570 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..1444
; US-08-116-247-6

Query Match: 59.2%; Score 940.8; DB 2; Length 1570;
Best Local Similarity 77.2%; Pred. No. 3.2e-265;

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9411089.7
 FILING DATE: 03-JUN-1994
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1572 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 -08-353-400-23

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REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
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LOCATION: 1..1418
FEATURE:
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LOCATION: 1..57
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1418
OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY"
OTHER INFORMATION: CHAIN"
US-08-793-450-7

Query Match 41.0%; Score 651.2; DB 4; Length 1418;
Best Local Similarity 67.5%; Pred. No. 1.4e-180;
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709 TGTCTACCCAGCCAGCAGCAGCGGTGGAGCAAAAAAATTGAGCCCGGCGCCATT 768

RESULT 7

US-08-467-420A-49

Sequence 49, Application US/08467420A

Patent No. 5683892

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.

APPLICANT: Appelbaum, Edward R.

APPLICANT: Chaiken, Irwin M.

APPLICANT: Cook, Richard M.

APPLICANT: Gross, Mitchell S.

APPLICANT: Holmes, Stephen D.

APPLICANT: McMillan, Lynette J.

APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

TREATMENT OF IL5 Mediated Disorders

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P. O. Box 1539-UM2220

CITY: King of Prussia

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RESULT 7

US-08-467-420A-49

Sequence 49, Application US/08467420A

Patent No. 5683892

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.

APPLICANT: Appelbaum, Edward R.

APPLICANT: Chaiken, Irwin M.

APPLICANT: Cook, Richard M.

APPLICANT: Gross, Mitchell S.

APPLICANT: Holmes, Stephen D.

APPLICANT: McMillan, Lynette J.

APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

TREATMENT OF IL5 Mediated Disorders

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P. O. Box 1539-UM2220

CITY: King of Prussia

dbb 2357 ATGCATGAGGCTGTGCACACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGTAAG 2416
QY 1467 TGAGCTCAG 1475
db 2417 TGAGTGTAG 2425

RESULT 10

JS-08-940-371-49

Sequence 49, Application US/08940371

Patent No. 5851525

GENERAL INFORMATION:

APPLICANT: Ames, Robert S.

APPLICANT: Appelbaum, Edward R.

APPLICANT: Chalken, Irwin M.

APPLICANT: Cook, Richard M.

APPLICANT: Gross, Mitchell S.

APPLICANT: Holmes, Stephen D.

APPLICANT: McMillan, Lynette J.

APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in

TREATMENT OF IL5 Mediated Disorders

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: P. O. Box 1539-0W2220

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/940,371

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/470,110

FILING DATE:

APPLICATION NUMBER: US 08/363131

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34,028

REFERENCE/DOCKET NUMBER: P50282

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610 270-5024

TELEFAX: 610 270-5090

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 6285 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

S-08-940-371-49

Query Match 40.1%; Score 637.4; DB 2; Length 6285;
Best Local Similarity 68.2%; Pred. No. 3.3e-176;
Matches 947; Conservative 0; Mismatches 406; Indels 36; Gaps 3;

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y 150 ACCTGCACAGCTCTCTGTTCTCATTAAGTACGTATGTTGTTACACTGGGTTCTGTCAGTCT 209
b 1130 ACCTGCACAGCTCTCTGTTCTCATTAAGTACGTATGTTGTTACACTGGGTTCTGTCAGTCT 209

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 2417 TGAGTGTAG 2425

SULT 12

T-US95-17082A-49
Sequence 49, Application PC/TUS9517082A
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATING ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:

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1047 ATCCAGCAGCAGGAGTGGATGAGTGGCAAGAGGTTCAAATGCAAGGTCAACACAAAGAC 1106
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1997 GTCTGCAGCAGGAGTGGCTGAATGGCAAGAGTACAAAGTCAAGGTCTCCAAACAAGCC 2056
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1407 AGCAGGAGTCTGAATAATTAATCTACTGAAGAAAGACCACTCTCCCGTCTCCCGGTAAA 1466
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2357 ATGATGAGGCTGTGCACACCACTACAGGAGAAAGAGCCCTCTCCCTGTCTCCCGGTAAG 2416
1467 TGAGCTCAG 1475
1111 1111
2417 TGAGTGTAG 2425

SULT 13

-08-488-376-17

Sequence 17, Application US/08488376

Patent No. 5811524

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter

APPLICANT: CHAMAT, Soulaïma Salim

APPLICANT: PAN, Li-Zhen

APPLICANT: WALSH, Edward E.

APPLICANT: HEARD, Cheryl Janne

APPLICANT: NEWMAN, Roland Anthony

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,376

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-150

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1428 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1428

; US-08-488-376-17

Query Match 40, 08; Score 634.6; DB 1; Length 1428;

Best Local Similarity 67.68; Pred. No. 1e-175;

Matches 965; Conservative 0; Mismatches 429; Indels 33; Gaps 4;

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QY 115 CTGCGCTAGTGCAGCCCTCAGAGAGCCTGTCCATCAGCTGCAGCAGTCTCTGTTTCTCAT 174
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, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/634,224
, FILING DATE:
, CLASSIFICATION: 424
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/488,376
, FILING DATE: 07-JUN-1995
, ATTORNEY/AGENT INFORMATION:
, NAME: Teskin, Robin L.
, REGISTRATION NUMBER: 35,030
, REFERENCE/DOCKET NUMBER: 012712-150
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (703) 836-6620
, TELEFAX: (703) 836-2021
, INFORMATION FOR SEQ ID NO: 17:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 1428 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: DNA (genomic)
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 1..1428
, PS-08-634-224-17

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-770-916-1

Perfect score: 1598

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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	933	58.8	1581	14	Monoclonal antibody
6	885	55.7	7528	22	Monoclonal antibody
7	801.8	50.5	1341	10	Bicistronic idiotype
8	768.2	48.4	1431	22	Chimeric antibody
9	768.2	48.4	1431	22	Chimeric 4H6 anti-

10	740.8	46.6	1676	23	ABI99041
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18	684.8	43.1	2053	23	ABI99029
19	684.8	43.1	2059	23	ABI99032
20	683.6	43.0	1347	11	AAQ5708
21	680.8	42.9	1347	17	AAT13733
22	670.6	42.2	1398	24	AA597062
23	662	41.7	1516	24	AAQ29308
24	656.8	41.4	1634	21	AAZ50012
25	654.6	41.2	1798	21	AAC98420
26	651.8	41.0	1567	22	AAC66522
27	651.2	41.0	1418	17	AAT26889
28	648.8	40.9	1392	19	AAV70129
29	648.8	40.9	1392	21	AAV72108
30	648.8	40.9	1392	21	AAAL1546
31	648.8	40.9	1392	24	ABL45925
32	648.8	40.9	1392	24	ABL48668
33	647.6	40.8	1431	17	AAT18059
34	643.6	40.5	1644	22	AA522593
35	638.8	40.2	1413	21	AA468898
36	638.6	40.2	1430	24	AAK98701
37	637.4	40.1	6285	19	AAV03503
38	636.6	40.1	1708	24	AA599474
39	636.2	40.1	1428	18	AA61241
40	635.8	40.0	6285	17	AAT34109
41	635.4	40.0	1386	14	AAQ53429
42	635	40.0	1673	24	AA599476
43	630.8	39.7	1431	18	AAT62513
44	630.8	39.7	1431	19	AAV35489
45	630.8	39.7	1431	24	AA517447

ALIGNMENTS

RESULT 1

ABL56968

ID ABL56968 standard; cDNA; 1389 BP.

AC ABL56968;

XX

XX

XX

DT 15-JUL-2002 (first entry)

XX

DE Recombinant 4G10 antibody heavy chain-6His coding sequence.

XX

KW Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer;

KW diagnosis; gene; ss.

XX

OS Unidentified.

OS Synthetic.

XX

XX

FH Key

FT CDS

FT

FT

FT

FT

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Location/Qualifiers

1..1389

/tag= a

/product= "4G10 heavy chain-hexahistidine"

/partial

/note= "The CDS does not include a start codon"

WO200218443-A2.

07-MAR-2002.

30-AUG-2001; 2001WO-US26926.

01-SEP-2000; 2000US-0653755.

(UPST-) UPSTATE BIOTECHNOLOGY INC.

Esinger D, Stiles L, Lamarche A, Jelinek T;

WPI; 2002-393728/42.
P-PSDB; ABB76126.

Novel recombinant monoclonal antibody with 4G10-hybridoma type specificity useful in diagnostic procedures, especially for detection of phosphotyrosine-containing proteins in a sample

Example; Page 54; 60pp; English.

The present sequence is the coding sequence for the heavy chain of a recombinant monoclonal antibody having 4G10 hybridoma-type specificity. The 3' region of the coding sequence comprises a sequence encoding a histidine tag, and was introduced into the 4G10 heavy chain cDNA by site-directed mutagenesis using the oligonucleotide given in ABL56973. The amended heavy chain cDNA was cloned into a eukaryotic vector and, with a vector for the 4G10 light chain, was used to produce a tagged, secreted, functional recombinant monoclonal antibody in transfected mammalian cells. The recombinant antibody is useful for detecting the presence of phosphotyrosine-containing proteins in a sample, for use in biological/medical research, in diagnosis of a variety of diseases including cancers, to identify cellular substrates for tyrosine kinases, for affinity purification of phosphotyrosine proteins and for determining the tyrosine phosphorylation status of one or multiple proteins in a given cell or tissue sample.

Sequence 1389 BP; 369 A; 395 C; 335 G; 289 T; 1 other;

Query Match	68.3%;	Score 1084;	DB 24;	Length 1389;
Best local Similarity	87.2%;	Pred. No. 3.1e-256;		
Matches 1218;	Conservative 1;	Mismatches 156;	Indels 21;	Gaps 2;
91	AGGTGACGCTGAAGCAGTCCAGGACCTGGCCCTGAGTGCAGCCCTCCACAGAGCCCTGCCATCA	150		
2	AGGTCCAGCTGCACGCTCTGGACCTGAACTGGTGAAGCCTGGGCTTCAGTGATGATAT	61		
151	CCTGCACAGTCTCTGGTTTCATTAATAGTAGTATGTTGATACATGGTGGTTCGTGAGTCTC	210		
62	CCTGCAGGACTTCTGCATACACATTCATCACTGAAACACCCGCTGCACCTGGTGAAGCAGAGCC	121		
211	CAGGAAGGGTCTGAGTGGCTGGAGTGCATATGAGT---GGTGGAGACACAGACTATA	267		
122	ATGGAGAGAGCCTTGAGTGGATTTGAGGATTAATCTTACTATGTTGGTCTTATCTTCA	181		
268	ATGACGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATCCCAAGGCCAACCTCTTCT	327		
182	GCCTGAAGTTCAAGGGCAAGGCCACATTTGACTGTAGACAAAGTCTCCAGCAGACCTACA	241		
328	TTAAATGAACAGTCTGGGAGTCTACTGCACAGCCATATATTTACTGTGCCAAGAAATAGAG	387		
242	TGGAGCTCCGAGCCTGACATCTGAGGATTTCTGAGTCTATTACTGTCAAGAGGGCTG	301		
388	GGGATATTTACTATGATTTTACTATTATGCCATGGACTACTGGGGTCAAGAACCTCAGTCA	447		
302	GGG-----CGTACTACTTTGACTTGTGGGCGCAAGGCCACCTCTCA	343		
448	CGGTCTCTCAGCCAAAACACACCCCATCATCTATTCACCTGGCCCTGGGTGGAG	507		
344	CAGTCTCTCAGCCAAAACACACCCCATCATCTATTCACCTGGCCCTGGGTGGAG	403		
508	ATACAACTGGTTCTCTCCGCTGACTCTGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCAG	567		
404	ATACAACTGGTTCTCTCCGCTGACTCTGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCAG	463		
568	TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCC	627		
464	TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCTCTCC	523		
628	TGACTGTGAGTCTTACACTATGACAGCTCAGTGCATGCTCCCTCCAGCAGCTGGCCNA	587		

Db	524	TGCAGTCTGGACTCTACACTATGACAGCTCAGTGTCTCCCTCCAGCACCTGGCCAA	583
Qy	588	GTCAGACCGTCACTGCGAGCGTTGCTCACCAGCCAGCAGCAGCGGTGGACAAAAC	747
Db	584	GTCAGACCGTCACTGCGAGCGTTGCTCACCAGCCAGCAGCAGCGGTGGACAAAAC	643
Qy	748	TTGAGCCAGCGGGCCCATTTCAACAATCAACCCCTGCTCCCTCCATGCAAGGAGTGTACA	807
Db	644	TTGAGCCAGCGGGCCCATTTCAACAATCAACCCCTGCTCCCTCCATGCAAGGAGTGTACA	703
Qy	808	AATGCCAGCTCCTAACTGAGGCTGAGGATACAGCTCCGCTCTTCATCTTCCCTCAAAATACA	867
Db	704	AATGCCAGCTCCTAACTGAGGCTGAGGATACAGCTCCGCTCTTCATCTTCCCTCAAAATACA	763
Qy	868	AGGATGTACTCATGATCTCCCTGACACCCAGAGTACCTGTGTGGTGGTGTGAGCGG	927
Db	764	AGGATGTACTCATGATCTCCCTGACACCCAGAGTACCTGTGTGGTGGTGTGAGCGG	823
Qy	928	AGGATGACCCAGAGCTCCAGATCAGCTGGTTTGTGAACAAGCTGGAAGTACACACAGCTC	987
Db	824	AGGATGACCCAGAGCTCCAGATCAGCTGGTTTGTGAACAAGCTGGAAGTACACACAGCTC	883
Qy	988	AGACAAAACCATAGAGAGGATTAACAACAGTACTATCCGGGTGCTCAGCAGCCCTCCCA	1047
Db	884	AGACAAAACCATAGAGAGGATTAACAACAGTACTATCCGGGTGCTCAGCAGCCCTCCCA	943
Qy	1048	TCCAGCACCGAGGACTGGATGAGTGGCAAGGAGTTCAAAATGCAAGTCAACAACAAGACC	1107
Db	944	TCCAGCACCGAGGACTGGATGAGTGGCAAGGAGTTCAAAATGCAAGTCAACAACAAGACC	1003
Qy	1108	TCCCATCACCATCCAGAGAACCATCTCAAAATTAAGGGCTAGTCAGAGCTCCACAAG	1167
Db	1004	TCCCATCACCATCCAGAGAACCATCTCAAAATTAAGGGCTAGTCAGAGCTCCACAAG	1063
Qy	1168	TATACATCTTGGCGCCACCCAGCAGAGCAGTGTCCAGGAAAGATGTCAGTCTCACTTGC	1227
Db	1064	TATACATCTTGGCGCCACCCAGCAGAGCAGTGTCCAGGAAAGATGTCAGTCTCACTTGC	1123
Qy	1228	TGGTGTGGCTTCAACCTGGAGACATCAGTGTGGAGTGGACACAGCAATGGGCATACAG	1287
Db	1124	TGGTGTGGCTTCAACCTGGAGACATCAGTGTGGAGTGGACACAGCAATGGGCATACAG	1183
Qy	1288	AGGAGAACTACAAGGACACCCAGCAGCTCTGGAGTCTGACGGTCTTACTTCAATATA	1347
Db	1184	AGGAGAACTACAAGGACACCCAGCAGCTCTGGAGTCTGACGGTCTTACTTCAATATA	1243
Qy	1348	GCAAGCTCAATATGAACAACCAAGTGGGAGAAACAGATTCTCTCATGCAAGCTGA	1407
Db	1244	GCAAGCTCAATATGAACAACCAAGTGGGAGAAACAGATTCTCTCATGCAAGCTGA	1303
Qy	1408	GACAGAGGGTCTGAAAATTAATACCTGAAAGAACCATCTCCGGTCTCCGGGTAAAT	1467
Db	1304	GACAGAGGGTCTGAAAATTAATACCTGAAAGAACCATCTCCGGTCTCCGGGTAAAG	1363
Qy	1468	GAGCTCAGCACCCACA 1483	
Db	1364	GTGGCCATCACCACCA 1379	

RESULT 2
ABL56966
ID ABL56966 standard; cdna; 1365 BP.
XX ABL56966;
XX
XX
XX 15-JUL-2002 (first entry)
XX Recombinant 4G10 antibody heavy chain coding sequence.
XX Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer;
XX diagnosis; gene; ss.
XX
OS Unidentified.

Db 397 TATTCTGTGCAAGAGCTATGGGGCTAGGGCTACACTTT-----TGGACTAC 444
QY 426 TGGGTCAAGAAACCTCAGTCACCGTCTCCTCAGCAAAACACACCCCAACCTCAGTCTAT 485
Db 445 TGGGCCAAGCACCACCTCTCACAGTCTCCTCAGCAAAACACACCCCAACCTCAGTCTAT 504
QY 486 CACTGGCCCTCGGTGTGGAGATACAACTAGTCTCCTCGTACCTCTGGGATCGCTGGTC 545
Db 505 CACTGGCCCTCGGTGTGGAGATACAACTAGTCTCCTCGTACCTCTAGGATCGCTGGTC 564
QY 546 AAGGCTACTTCCCTGAGTCAGTCTGACTTGGAACTCTGGATCCTCTCCAGCAGT 605
Db 565 AAGGCTTATTTCCCTGAGCCAGTCTGACTTGGAACTCTGGATCCTCTCCAGTCT 624
QY 606 GTGCACACTTCCAGCTCTCTCGAGTCTGGACTTACACTATGAGCAGCTCAGTGACT 665
Db 625 GTGCACACTTCCAGCTCTCTCGAGTCTGGACTTACACTTACCTCAGCAGCTCAGTGACT 684
QY 666 GTCCCTCCAGCCTTGGCCAAAGTACAGCCTGACCTCAGCGTGTCTCAGCCAGCCAGC 725
Db 685 GTAACTCGAGCCTTGGCCAGCAGTCTCAGTCTGAGTGGCCCAACCCGCAAGC 744
QY 726 AGCAGCAGGTGGACAAAACCTTGGAGCCCAAGCGGCCATTTCAACAATCAACCCCTGT 785
Db 745 AGCAGCAGGTGGACAAAACCTTGGAGCCCAAGCGGCC-----ACAATCAAGCCCTGT 798
QY 786 CCTCATGCAAGGAGTGTCAAAATGCCCCAGCTCTTAACCTCGAGGTGGAGCCTCCTC 845
Db 799 CCTCATG-----CAAAATGCCCCAGCCTTAACTCTTGGTGGACCATCCCTC 846
QY 846 TTCACTTCTCCCTCAAAATATCAAGAGTACTCTATGATCTCCCTGACACCCCAAGGTACG 905
Db 847 TTCACTTCTCCCTCAAAAGATCAAGATGATCTATGATCTCCCTGAGCCCATAGTACAA 906
QY 906 TGT 965
Db 907 TGT 966
QY 966 AACTGTGAAGTACACAGCTCAGACAAACCCATAGAGAGGATTACACAGTACTATC 1025
Db 967 AACTGTGAAGTACACAGCTCAGACAAACCCATAGAGAGGATTACACAGTACTATC 1026
QY 1026 CGGT 1085
Db 1027 CGGT 1086
QY 1086 TGAAGGTCAACAAAGAGCTCTCCATCACCCTCGAGAGAACCTCTCAAAATTA 1145
Db 1087 TGAAGGTCAACAAAGAGCTCTCCAGCGCCCTCGAGAGAACCTCTCAAAACCCCAA 1146
QY 1146 GGGT 1205
Db 1147 GGGT 1206
QY 1206 AAGATGT 1265
Db 1207 AAGATGT 1266
QY 1266 TGGACAGCAATGGGCATACAGAGAGAACTACAAAGACACCCAGCAGTCTCTGGACTCT 1325
Db 1267 TGGACAGCAATGGGCATACAGAGAGAACTACAAAGACACCCAGCAGTCTCTGGACTCT 1326
QY 1326 GAGGT 1385
Db 1327 GAGGT 1386
QY 1386 GATTCCTTCTCATGCAAGTGTGAGACAGGGGTCTGAAATTAATTAACCTCAAGAGAGC 1445
Db 1387 AATAGCTTACTCTGT 1446
QY 1446 ATCTCCGGGTCTCGGGTAATAGCTCAGCAGCCCAACAAAGCTCTCAGAGCTCTAAGAG 1505
Db 1447 TTCTCCGGGTCTCGGGTAATAGCTCAGCAGCCCAACAAAGCTCTCAGAGCTCTAAGAG 1506

QY 1506 ACTGGCACCACCATATCCATCCATCCCTTGTATAAATAAAGCATCCAGCAAGCTGTGTACC 1565
Db 1507 ACCCAGCTCATCTCCATGCTTCCCTTGTATAAATAAAGCATCCAGCAGCTGTGTGGACC 1566
QY 1566 ATGTAAAAA 1580
Db 1567 ATGTAAAAA 1581

RESULT 6

AAF30316
ID AAF30316 standard; cDNA; 7528 BP.

XX AAF30316;

AC AAF30316;

XX 14-MAY-2001 (first entry)

DT 14-MAY-2001 (first entry)

XX Bicistronic idiotype plasmid VRI642.

DE AAF30316

XX Fms-like tyrosine kinase; mouse; human; vaccine;

KW immunotherapy; therapy; tumour; lymphoma; gene therapy; VRI642;

KW plasmid VAXID; antibody; idiotype; vector; ss.

XX Chimeric - Cytomegalovirus.

OS Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

OS Chimeric - Bos taurus.

XX WO200109303-A2.

XX 08-FEB-2001.

PD 31-JUL-2000; 2000WO-US20679.

XX 30-JUL-1999; 99US-0146170.

XX (VICA-) VICAL INC.

XX Hermanson GG;

XX WPI; 2001-123319/13.

DR Immunogenic compositions comprising Flt-3 ligand encoding

XX polynucleotide and one or more antigen, or cytokine encoding

PT polynucleotides, useful for suppressing tumour growth and for treating

PT autoimmune diseases (e.g. rheumatoid arthritis) -

XX Example 2; Page 101-106; 149pp; English.

PS The present sequence is that of patient-specific bicistronic

XX chimeric idiotype VRI642 (plasmid VAXID), which is used to treat

CC B-cell lymphoma patients. The plasmid includes the cytomegalovirus

CC immediate-early promoter, enhancer and 5' untranslated sequences,

CC driving the expression of mouse-human chimeric immunoglobulin

CC light and heavy chain sequences. The human light and heavy chain

CC variable regions are derived from B-cell lymphoma cell line RAMOS.

CC The transcriptional terminator region includes polyA and termination

CC signals from the bovine growth hormone gene. According to the

CC invention, co-administration of VRI642 with a plasmid (see AAF30314)

CC encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a

CC means of treating a patient with B-cell lymphoma.

XX Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;

SQ Query Match

Best Local Similarity 55.7%; Score 885; DB 22; Length 7528;

Matches 1116; Conservative 0; Mismatches 295; Indels 24; Gaps 3;

QY 41 CTGGGGGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 100

Db 1246 CCTGTGTTCT 1305

QY 210 CCAGGAAAGGCTGCTGAGTGGCTGGAGTGATATGGA---GTGGTGAGACACAGACTAT 266
Dp 121 CCAGGAAAGGCTTAAAGTGGATGGCTGATTAACACACCTACATACAGAAACCAACATAT 180
QY 267 AATGAGCTTTTCATATCCAGACTGAGCATCAGCAAGCAAAATTCRAAGAGCCAACTCTTC 326
Dp 181 GCTGATGACTTCAAGGAGCGTTTGCCTTCTCTTGGAAACCTCTGCCAGCAGTGCCTTT 240
QY 327 TTTTAAATGAACAGCTGCTGAGCTACTGACAC---AGCCATATATTACTGTGCAGAAAT 383
Dp 241 TTGCGATTCACACACCTCAGAAATATGAGACTATGGCTACATATTTCTGTGAAGA--- 297
QY 384 AGAGGGATATTTACTATGATTTACTTACTTATGATGACTGAGTGGGTCAAGGAACTCA 443
Dp 298 -----TTTATTTCTAAGGGGACTACTGGGTCAAGGAACTCA 336
QY 444 GTCACGGTCTCTCAGCCAAACACACACCCCATCAGTCTATCCACTGCCCCGTGGTGT 503
Dp 337 GTCACGGTCTCTCAGCCAAACACACACCCCATCAGTCTATCCACTGCCCCGTGGTGT 396
QY 504 GGAGATACAACTGTTCTCTCGTACTCTGGATGCTGGATGCTGGTCAAGGGCTACTTCCCTGAG 563
Dp 397 GGAGATACAACTGTTCTCTCGTACTCTGGATGCTGGATGCTGGTCAAGGGTATTTCCTGAG 456
QY 564 TCAGTACTGCTGACTTGGAACTCTGATCCCTGTCCAGCAGTGTGCACACCTTCCAGCT 623
Dp 457 CCAGTGACCTTGACCTGGAACCTCTGATCCCTGTCCAGTGTGTGCACACCTTCCAGCT 516
QY 624 CTCCTGAGCTGAGCTTACACTATGACAGCTCAGTACTGTCCCTCCAGCACTGG 683
Dp 517 GTCTGCTGAGCTGACCTTACACCCCTCAGCAGCTCAGTACTGTAAGCTCGAGCACTGG 576
QY 684 CCAAGTACAGCGTCACTGTCAGCGCTTGTCTACCCAGCAGCAGCAGCAGTGGACAAA 743
Dp 577 CCCAGCCAGTCCATCAGCTGAAATGTGCCACCCAGCAGCAGCAGCAGTGGACAA 636
QY 744 AAATTTGAGCCAGCGGCCCATTTCAACAATCAACCCCTGCTCCATGCAAGAGTGT 803
Dp 637 AAATTTGAGCCAGCGGCC-----ACAATCAAGCCCTGCTCCATG----- 680
QY 804 CACAATCCAGCTCTTAACCTCAGGCTGGACCATCCGCTTTCATCTTCCCTCCAAAT 863
Dp 681 --CAATCCAGCAGCACTAACCCTTGGTGGACCATCCGCTTTCATCTTCCCTCCAAAG 738
QY 864 ATCAAGGATGACTCATGATCTCCCTGACACCCAAAGTCACTGTGTGGTGGATGTG 923
Dp 739 ATCAAGGATGACTCATGATCTCCCTGACGCCCATAGTACATGTGTGTGGTGGATGTG 798
QY 924 AGCGAGGATGACCCAGAGCTCCAGATCAGCTGTTTGTGAACAACCTGGAAGTACACACA 983
Dp 799 AGCGAGGATGACCCAGAGTGTCCAGATCAGCTGTTTGTGAACAACCTGGAAGTACACACA 858
QY 984 GCTCAGACACAAACCCATAGAGAGATTACACAGTACTATCCGGTGGTTCAGACCCCTC 1043
Dp 859 GCTCAGACACAAACCCATAGAGAGATTACACAGTACTTCCGGTGGTTCAGTCCCTC 918
QY 1044 CCAATCCAGCAGCAGCTGATGAGTGGCAGGAGTTCAAAATGCAAGTCAACAACAAA 1103
Dp 919 CCAATCCAGCAGCAGCTGATGAGTGGCAGGAGTTCAAAATGCAAGTCAACAACAAA 978
QY 1104 GACCTCCCATCCCATCAGAGAACCACTCTCAAAATTAAGGGCTAGTCAGAGCTCCA 1163
Dp 979 GACCTCCAGCAGCAGCTCAGAGAACCACTCTCAAAACCAAGGCTAGTGAAGCTCCA 1038
QY 1164 CAAGTATACATCTTGGCCGCCACCCAGCAGAGTGTGTCAGGAAAGATGTCTAGTCTACT 1223
Dp 1039 CAGGTATATGCTTTCCTCCACCAAGAAAGAGATGACTAAGAAACAGCTCACTGTACC 1098
QY 1224 TGCCTGGCTGGGCTTCAACCCCTGGACATCAGTGTGGAGTGGACAGCAATGGGCAT 1283
Dp 1099 TGATGCTCAGAGCTTCAATGCTTGAAGACATATACGTGGAGTGGACCAACCAAGGAAA 1158
QY 1284 ACAGAGGAGAACTACAAGGACACCCAGCTGCTGGACTCTGAGGGTCTTACTTCTATA 1343

Db 1159 ACAGAGCTAACTACAAGAACTGAACTGAACTGCTGAGCTCTGATGTTCTTACTCATG 1218
QY 1344 TATAGCAAGCTCAATATGAAACAAAGCAAGTGGGAGAAACAGATTCCTTCTCATGCAAC 1403
Dp 1219 TAGAGCAAGCTGAGAGTGGAAAGAGAGACTGGGTGGAAAGAAATAGCTACTCTCTTCA 1278
QY 1404 GTGAGACACAGAGGCTGTGAAATAATTACTCTCAAGAAGACCATCTCCCGGTCTCCGGGT 1463
Dp 1279 GTGGTCCAGGAGGCTGTGCAATATCCACACACTAAGAGCTTCTCCCGGACTCCGGGT 1338
QY 1464 AAA 1466
Dp 1339 AAA 1341
RESULT 8
AAC91017
ID AAC91017 standard; DNA: 1431 BP.
XX
AC AAC91017;
XX
DT 15-MAR-2001 (first entry)
XX
Chimeric 4H6 anti-DR4 antibody heavy chain DNA.
XX
Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
KW autoimmune; ds.
XX
Homo sapiens.
OS Synthetic.
XX
W0200073349-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US14599.
XX
PR 28-MAY-1999; 99US-0322875.
XX
(GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;
XX
WPI; 2001-041145/05.
XX
Novel anti-death receptor 4 antibodies useful for treating cancer and
PT immune related disorders such as rheumatoid arthritis, sjogren's
PT syndrome, Grave's disease and diabetes mellitus -
XX
PS Disclosure; Fig 18; 126pp; English.
XX
CC The present invention relates to an anti-death receptor 4 (DR4)
CC antibody. The antibodies of the invention are useful for inducing
CC apoptosis in mammalian cancer cells such as colon cancer cells and
CC for treating an immune-related disease in a mammal such as arthritis
CC and autoimmune disease.
XX
SQ Sequence 1431 BP; 350 A; 438 C; 367 G; 273 T; 3 other;
Query Match 48.4%; Score 768.2; DB 22; Length 1431;
Best Local Similarity 72.8%; Pred. No. 1e-178;
Matches 1043; Conservative 3; Mismatches 351; Indels 36; Gaps 3;
QY 52 TCTTCTGCTGCTGATATCCCAAGTGTGTCTATCCAGGTGCAAGTCAAGCTCAG 111
Dp 20 TCTTCTTCTTCTAGTCAACTGCACTGGAGTACATTCASARCTKCACTGAGGAGTCA 79
QY 112 GACCTGGCTACTGAGCCCTCAGAGCCTTCCATCATCCCTGACAGTCTCTGTTTCT 171
Dp 80 GACCTGGCTGCTGGCGCCCTCAGAGCCTTCCATCATCTTGCATCTCTCTGGGTTTT 139
QY 172 CATTAACCTAGCTATGGTGTACACTGGTTCGTCTCCAGAAAGGCTCTGGAGTGC 231

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140 CATTAAACAGATATGGGTACATCGGTTCCAGCCTCCAGGAAGGCTCGAGTGGC 199
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
232 TGGAGTGAATATGGAGTGGTGACACAGACTATAATGACAGTTCATATATACAGACTCA 291
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
200 TGGAGTAATATGGCTGTGGAGACCAAAATTAATTCGGCTCATGTCCAGACTGA 259
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
292 GCATCAGCAGGACAAATCCAAAGAGCCAACTCTCTTTAAATGAACAGTTCGAGCTA 351
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
260 GCATCAGCAAGACAACTCCAAAGAGCCAAAGTTTCTTAAATAATGAACAGTCTGCAAACTG 319
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
352 CTGACAGCAGCATATATATCTGTCGAGAAATAGAGGGATATTTACTATGATTTCACT- 410
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
320 ATGACAGAGCCATGACTACTGTCGAGAGAGGGGAATTCGATTACTACGGTATGATG 379
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
411 -----TATGCCATGCACTACTGGGTCAGGAACTCAGTCAACCGTCTCCTCAG 459
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
380 TCCTATCTTACCATTTATGAATCTTGGGTCAAGGAACCTCAGTCAACCGTCTCCTCAG 439
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
460 CCAAAACACACCCCATCAGTCTATCCACTGGCCCTGGGTGGAGATACAACTGGTT 519
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
440 CCAAAACAGGGGCCATCGGTCTCCCTCGGCACCTCTCCAGAGACCTCTGGG 499
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
520 CCTCGTGACTCTGGGATGCTGTCAAGGGCTACTCTCCCTGAGTCACTGACTGT 579
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
500 GCACAGCGCCCTGGGTGCTGTCAAGGACTACTTCCCGAACCGGTGAGGTGCTG 559
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
580 GGAATCTGGAGTCCCTGTCAGCAGTGTGCACACCTTCCAGCTCTCTGAG---TCTG 636
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
560 GGAATCTAGGCGCCTGACAGCGCGTGCACACCTTCCCGCTCTCTACAGTCTCTCAG 619
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
637 GACTCTACACTATGAGCAGCTCAGTACTGTCCCTCCAGCAGCTGCGCAAGTACAGCG 696
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
620 GACTCTACTCTCCTCAGCAGCTGTGTGCTCTCTAGCAGCTTGGGCAACCCAGACT 679
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
697 TCACCTGAGCGTGTCTCACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 756
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
680 ACATCTGAAGTGTAATCAGAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 737
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
757 GCGGGCCCATTTCAACAATCAACCCCTGTCTCTCCATCAAGAGAGTGTCAAAATCCCA 816
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
738 -----CAATCTTGACAAAACTCACACATGCCACCGTCCCGCCAG 778
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
817 CTCCTAACCTGAGGCTGACCATCTCGTCTCATCTCTCCCTCCAAATATCAAGGATGAC 876
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
779 CACCTGAATCTCTGGGGGAGCGTCACTGCTCTCTCTCCCGCCAAACCCCAAGSACACC 838
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
877 TCATGATCTCCCTGACACCCCAAGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 936
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
839 TCATGATCTCCCGGACCCCTGAGGTGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 898
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937 CAGAGCTCCAGATCAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 996
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
899 CTGAGTCAAGTTCATCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 958
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
997 CCATPAGAGAGATTACAACTAGTATATCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1056
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
959 CGCGGGAGGAGCAGTACAAACAGCAGTACCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1018
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1057 AGGATGTAGTGTGAGGAGTTCATATGCAAGTCAACAAAGACCTCCCATCATC 1116
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1019 AGGATGTGTGAATGCGAAGGAGTACATGTGCAAGTCTTCAACAAAGACCTCCCATCATC 1078
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1117 CCATCAGAGAACCACTCAAAAATTAAGGGCTAGTCAAGCTCCCAAGTATATCATCT 1176
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1079 CCATCAGAGAACCACTTCCAAAGCCAAAGGGCAGCCCGGAGAACCAAGGTGTACACC 1138
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1177 TGCCGCCACACAGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1236
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1139 TGCCGCCATCCCGGAGAGATGACCAAGACCAAGGTGTACCTGCTGTGTGTGTGTGTGTGT 1198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1237 GCTTCAACCTTGAGACATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1296
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[illegible]

QY	1297	ACAAGGACACGCGACCAAGTCTCTGACGCTCTTACTTTCATATATAGCAAGCTCA	1355
Db	173	AAAAGACACGCGCTCCCGTGTGGAGTCCGAGCGCTCTTCTCTACAGCAAGCTCA	114
QY	1357	ATATCAAAACACGAAGTGGGAGAAACAGATTCCTTCTCATGCAACGCTGAGACACGAGG	1416
Db	113	CCGTGGGACAAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGCTCCGTCATGCATGAGG	54
QY	1417	GTCTGAAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGA	1469
Db	53	CTCTGCACACCACTACACGCAGAGAGCGCTTCCCCTGTCTCCGGGTAAATGA	1
RESULT 10			
ABI99041			
ID	ABI99041	standard; cDNA; 1676 BP.	
XX	AC	ABI99041;	
XX	DT	25-FEB-2002 (first entry)	
XX	DE	Murine PCB223 coding sequence.	
XX	KW	Mouse; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; antiinflammatory; antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus; ss.	
OS	OS	Syn SP.	
XX	OS	Synthetic.	
XX	PN	WO200170245-A1.	
XX	PD	27-SEP-2001.	
XX	PF	22-MAR-2001; 2001WO-US09616.	
XX	PR	22-MAR-2000; 2000US-191274P.	
PR	PR	15-MAY-2000; 2000US-204249P.	
PR	PR	23-JAN-2001; 2001US-264003P.	
XX	XX	(CORI-) CORIXA CORP.	
XX	XX	Carter D, Zhu S, Arimilli S, Wang A;	
PI	PI		
XX	XX		
DR	DR	WPI; 2001-616371/71.	
XX	XX	P-PSDB; ABB56471.	
XX	XX		
PT	PT	Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha and beta domain linked through amino acid linker and multimerization domain	
PS	PS	Disclosure; Page 115; 147pp; English.	
XX	XX		
CC	CC	The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha domain and a beta domain linked through an amino acid linker and a multimerization domain. The first and the second molecule are linked through the multimerisation domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence encodes a single chain MHC class II molecule of the invention.	
XX	XX		
SQ	SQ	Sequence 1676 BP; 438 A; 470 C; 407 G; 361 T; 0 other;	

Query Match	46.6%	Score 740.8	DB 23	Length 1676
Best Local Similarity	84.7%	Prod. No. 5.7e-172		
Matches	861	Conservative 0	Mismatches 137	Indels 18
Gaps	2			
456	TCAGCCAAAACACACACCCCATCAGTCTATCCACTGCGCCCTGGGTGTGGAGATACAAC	515		
457				
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516	GGTTCCTCGGTCTGGATCGCTGGTCAAGGGCTACTTCCTCAGTCAAGTCAAGTGTG	575		
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533	GGCTCCTCGGTGACTCTAGGATGGCTGGTCAAGGTTATTTCCCTGAGCCAGTGACCTTG	792		
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RESULT 11
AAF30341
ID AAF30341 standard; cDNA; 6729 BP.
XX
AC AAF30341;
CC
DT 14-MAY-2001 (first entry)
XX
DE Bicistronic idiotype plasmid VR1632.
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine; immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1632;
KW antibody; idiotype; vector; ss.
XX
OS Chimeric - Cytomegalovirus.
OS OS Chimeric - Mus musculus.
OS OS Chimeric - Bos taurus.
XX
PN WC200109303-A2.
XX
PD 08-FEB-2001.
XX
Pf 31-JUL-2000; 2000WO-US20679.
XX
PR 30-JUL-1999; 99US-0146170.
XX
PA (VICA-) VICAL INC.
XX
PI Hermanson GS;
XX
DR WPI; 2001-123319/13.
PT
XX Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS Example 2; Page 107-111; 149pp; English.
XX
CC The present sequence is that of bicistronic plasmid VR1632, which includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranslated sequences, driving the expression of mouse immunoglobulin kappa light and gamma 1 heavy chain constant regions. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene.
CC Tumour-specific variable regions from a patient can be PCR amplified and cloned into this vector to produce the patient's individual vaccine construct. The light and heavy chain variable regions from the B-cell lymphoma cell line RAMOS were amplified and cloned into VR1632 to provide test vaccine construct VR1642 (see AAF30316).
CC According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a means of treating a patient with B-cell lymphoma.
XX
SQ Sequence 6729 BP; 1727 A; 1744 C; 1629 G; 1629 T; 0 other;
Query Match 46.5%; Score 737.8; DB 22; Length 6729;
Best Local Similarity 84.3%; Pred. No. 4.7e-171;
Matches 861; Conservative 0; Mismatches 142; Indels 18; Gaps
Qy 449 CGTCTCCTCAGCGAAACCAACACCCTCATGTCATCCACTGGCCCCCTGGGTGGAGA
Db 2734 CGTCTCCTCGGCCAAACAGCGCGCCCCTATCCACTGGCCCCCTGTGTGGAGA
Oy 509 TACAAGTGTTCTCCTCGTGACTTCTGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCAGT
Db 2794 TACAAGTGCTCCTCGTGACTTAGGATGCTGTGTCAAGGGTTATTTCCTGAGCCAGT
Oy 569 GACTGTGACTTGGAATCTGGATTCCTGTGCAGCAGTGTGCACACCTTCCAGACTCTCTCT
Db 2854 GACCTTGACTGGAACTCTGGATCCTGTGTCAAGTGTGTGCACACTTCCAGCTGTCTCT

409 CTATGCGATGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAGCCAAACAA 468
|||||
424 ACGATGCTATGGACTACTGGGTCAGGACCTCAGTCACCGTCTCCTCAGCCAAACGA 483
|||||
469 CACCCCATCAGTCTATCCACTGCGCCCTGGGTGGAGATACAACTGGTCTCCCTGTA 528
|||||
484 CACCCCATCTGCTATCCACTGCGCCCTGGATGCTGCTGCCAACTAACTCCATGTTGA 543
|||||
529 CTCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
|||||
544 CCCTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
|||||
589 GATCCCTGCTCAGCAGTGTGACACCTTCCAGCTCTCCAGCTCTGCTGCTGCTGCTGCT 648
|||||
604 GATCCCTGCTCAGCAGTGTGACACCTTCCAGCTCTCCAGCTCTGCTGCTGCTGCTGCT 663
|||||
649 TGAGCAGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
|||||
664 TGAGCAGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
|||||
709 TTGCTCACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 768
|||||
724 TTGCCCACCCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 783
|||||
769 CAACAATCAACCCCTGCT 828
|||||
784 GTRAGCCTTGCAATG-----TACAGTCC 807
|||||
829 AGGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 888
|||||
808 CAGAAGTATCATCTGCT 867
|||||
889 TGACACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
|||||
868 TGACTCTTAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 927
|||||
949 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
|||||
928 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 987
|||||
1009 ATTACACAGTACTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
|||||
988 AGTTCAACAGCAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
|||||
1069 GTGCGAAGGAGTCAATGCAAGTCAACAGAGCTCCCATCCCATCCCATCCCATCCCAT 1128
|||||
1048 ATGCAAGGAGTCAATGCAAGTCAACAGAGCTCCCATCCCATCCCATCCCATCCCAT 1107
|||||
1129 CCATCTCAAAATTTAAAGGCTAGTCAAGAGTCCACAGATATACATCTTTCGCGCCAC 1188
|||||
1108 CCATCTCAAAATTTAAAGGCTAGTCAAGAGTCCACAGATATACATCTTTCGCGCCAC 1167
|||||
1189 CAGAGCAGTCTCCAGGAAAGATGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1248
|||||
1168 AGGAGCAGATGCGCAAGGATTAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1227
|||||
1249 GAGACATCAGTGTGGATGGACAGCAATGGGCATACAGAGGAGAGTACAGGACACCG 1308
|||||
1228 AAGACATTTACTGTGAGTGGCAGTGGATGGGCAGCCAGCCAGGAGAACTTACAGAAC 1287
|||||
1309 CACCAAGTCTGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1368
|||||
1288 AGCCCATCATGGACACAGATGGCTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1347
|||||
1369 GCAAGTGGGAGAAACAGATTTCTTCTCATGCAAGTGTGAGACAGAGGCTGTGAAAAAT 1428
|||||
1348 CCAACTGGGAGGCGAAGAAATTTACTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1407
|||||
1429 ACTACCTGAAGAAGACCATCTCCCGGTTCCCGGGTAAATGAGCTGACAGCCACAAAGCT 1488
|||||
1408 ACCATACTGAGAAGAGCCTCTCCCACTCTCTCTGTTAAATGATCCCACTGCTCCTTGG 1467
|||||
1489 CTCAGGTCTTAAGACACTGGGCAACCCCATATCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
|||||

Db 1468 CTCGTGCTTACAGGACTCTGACACCTTACCTCCACCCTCC-TGTATAATAAGCACC 1526
|||
QY 1549 CAGCAAAAGCCTGGTACCATGTAAAAAAGAAAAA 1588
|||
Db 1527 CAGCACTGCCTTGGGACCTGCAAAAAAAGAAAAA 1566
|||

RESULT 13
AAN40025
ID AAN40025 standard; DNA; 1528 BP.
XX AAN40025;
AC AAN40025;
XX 01-DEC-1991 (first entry)
DT
DE mRNA encoding gamma anti-carcinoembryonic antigen chain.
XX Immunoglobulin; ss mRNA; carcinoembryonic antigen chain.
KW
XX Key Location/Qualifiers
FT CDS 30..1430
FT /*tag= a
XX
XX EPI25023-A.
XX
XX 14-NOV-1984.
XX
XX 06-APR-1984; 84EP-0302368.
XX
XX 08-APR-1983; 83US-0483457.
XX
XX (CITY) CITY OF HOPE.
XX (GETH) GENENTECH INC.
XX
XX Cabilly S, Holmes WE, Wetzal RB, Heyneker HL, Riggs AD;
PI
XX WPI; 1984-283749/46.
XX P-PSDB; AAP40032.
XX
XX Immunoglobulin(s) produced by recombinant host cells - useful as
antibodies analogous to forms from mammals.
XX
XX Disclosure; Fig. 5A-B; 79pp; English.
XX
XX The mRNA is the coding sequence of the combined cDNA inserts of
recombinant vectors p gamma 298 and p gamma 11 (see AAN40024).
CC It encodes gamma anti-carcinoembryonic antigen chain. Using the
CC vectors the immunoglobulin is produced readily in pure monoclonal form.
CC Genetic manipulations can be used to produce chimeras of variants
CC drawing their homology from species differing from each other. Protein
CC manipulation is also possible.
XX
XX Sequence 1528 BP; 375 A; 443 C; 371 G; 339 U; 0 other;
SQ

Query Match 45.1%; Score 716.8; DB 5; Length 1528;
Best Local Similarity 54.2%; Pred. No. 4.3e-166;
Matches 819; Conservative 231; Mismatches 417; Indels 43; Gaps 4;
QY 55 TCTGCTGGTGACATTTCCCAAGCTGTGTCTTATCCAGGTGAGTGAAGCAGTCTCTGTTCTCAT 114
|||
Db 52 UUUACCUUGUCUGGUUU 111
|||
QY 115 CTGGCTAGTGGAGCCCTCAGCAGAGCCCTGTCATCCTGACAGTCTCTGTTCTCAT 174
|||
Db 112 GAGUCUUAUUGAGGCGGUGGUGCCUGAAACUCUCUGUGCAGCCUCUGAUUCACUU 171
|||
QY 175 TAACTAGTATGGTGTACATGCGTTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
|||
Db 172 UCAGUAGAUUGCCCAUGUCUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 231
|||
QY 235 GAGTATATGGTGTGGAGACACAGACTATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 291
|||

QY	1372	AGTGGGAGAAAA	CAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAATTACT	1433
Db	1333	ACUGGAGGGCAGAAAUACU	UUCACCUCCUGUCUGUUACAUGAGGGCCUGCAACAACCACC	1392
QY	1432	ACCTGAAGAAGACCATCTCCCGGTCTCCGGTAAATCAGCTCAGCACCCACAAGCTCTC	1491	
Db	1393	AUACUGAGAAGAGCCUCCUCCACUCUCUGUAAUAGUCCAGUGUCUUGAGGCCUC	1452	
QY	1492	AGTCTTAAGAGACACTGGCACCACATATCCATGCATCCCTTGTATATAAATGAAGCATCCAG	1551	
Db	1453	UGGUCCUACAGGACUCUGACACCUCCACUCCACCCUCCC	UGUAAUAAUAAAGCACCAG	1511
QY	1552	CAAAGCTGG	1561	
Db	1512	CACUGCCUUG	1521	
RESULT 14				
AAAN40024				
ID	AAAN40024 standard; DNA; 1528 BP.			
XX	AAAN40024;			
AC	XX			
AC	XX			
DT	01-DEC-1991 (first entry)			
XX	Combined cDNA inserts of p gamma 298 and p gamma 11 which encode			
DE	gamma anti-carcinoembryonic antigen chain.			
XX	Immunoglobulin; ds DNA; carcinoembryonic antigen;			
KW	vector p gamma 11; vector p gamma 298.			
XX	EP125023-A.			
PN	XX			
XX	14-NOV-1984.			
PD	XX			
XX	06-APR-1984; 84EP-0302368.			
PF	XX			
XX	08-APR-1983; 83US-0483457.			
PR	(CITY) CITY OF HOPE.			
XX	(GETH) GENENTECH INC.			
PA	XX			
PI	Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;			
DR	WPI; 1984-283749/46.			
XX	Immunoglobulin(s) produced by recombinant host cells - useful as			
PT	antibodies analogous to forms from mammals.			
PT	Disclosure; Fig. 5A-B; 79pp; English.			
XX	The sequence is the combined cDNA inserts of vectors p gamma 298			
CC	and p gamma 11. The sequence encodes gamma anti-carcinoembryonic			
CC	antigen chain. Using the vectors the immunoglobulin is produced readily			
CC	in pure monoclonal form. Genetic manipulations can be used to produce			
CC	chimeras of variants drawing their homology from species differing from			
CC	each other. Protein manipulation is also possible.			
XX	Sequence 1528 BP; 376 A; 443 C; 370 G; 339 T; 0 other;			
SQ	Query Match			
		44.9%;	Score 713.6;	DB 5; Length 1528;
		Best Local Similarity	69.4%;	Pred. No. 2.7e-165;
		Matches 1048;	Conservative	0; Mismatches 419; Indels 43; Gaps 4;
QY	55	TC TGCTGGTGACATCCCAAGCTGTGTCCTATCCAGGTGCAGCTGAAGCAAGTCCAGGAC	114	
Db	52	TTTACCTTCTCCTTGTTTTAAAGATTGCCAGTGAAGTGATGCTGGTGGAGTCTGGGG	111	
QY	115	CTGGCCTAGTCGAGCCCTCAGACAGCTGTTCATCACCTGCACAGTCTCTGGTTTCTCAT	174	
Db	112	GAGTCTTAATGGAGCTGGAGGGTCCCTGAAACTCTCTGTCAGCTCTGGATTCACTT	171	

CC also be biofarmed for the prodn. of anti-virus antibodies.

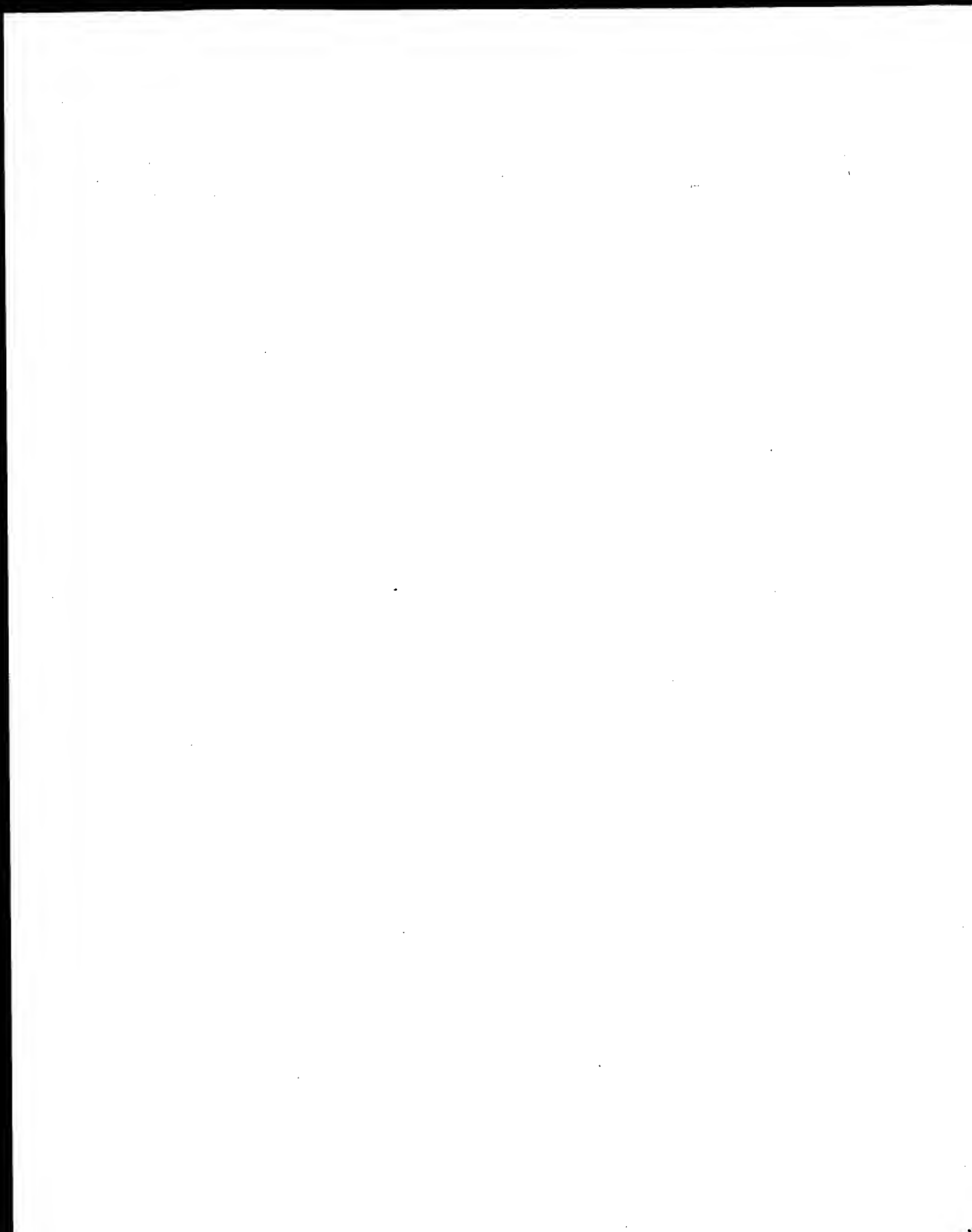
Sequence 1553 BP; 386 A; 450 C; 372 G; 345 T; 0 other;

Query Match 43.5%; Score 690.6; DB 16; Length 1553;
Best Local Similarity 67.7%; Pred. No. 1.2e-159;
Matches 1049; Conservative 0; Mismatches 454; Indels 46; Gaps 4;

16	AGAGCCCTCCATCAGAGCATGGCTGCTCTGGGGCTGCTCTTCTGCTGGTGCATTCGCCAA	75
39	AAACACTGACTCTAATCATGAATGTAACATGGATACCTTTCCTTTTATCTGTCGTAACCT	98
76	GCTGTGCTTATCCAGGTGAGTGAAGCAGTCCAGACCTGGGCTAGTGCAGCCCTCAC	135
99	CAGGTGCTACTACAGCTTCCAGTCCAGCAGTCTGGGGCTGAGCTGSCAAGACCTGGGG	158
136	AGAGCCCTGTCATCAGCTGACAGTCTCTGTTCTCATTAACCTAGTATGGTGTACACT	195
159	CTTCAGTGAAGTCTCTGTCGAAGCTTCTGGCTACACCTTTACTAGCTACTGGATGCACT	218
196	GGGTTCCTGCTCAGTCTCCAGGAAAGGTCTGGAGTGGCTGGGAGTATATGGAGTGS	252
219	GGGTAAACAGAGCCCTGGACAGGCTCGGAATGGATGGGGCTATTATCTGGAATG	278
253	GAGACACAGACTATATATGCACTTTTCATATCCAGACTGAGCATCAGCAAGGACAAATCCA	312
279	GTGATACTAGTACACTCAGAGTTCAGGCAAGGCCACATTCAGTCCAGATAAATCCT	338
313	AGAGCCAACTCTCTTAAATGAACAGTCTGGAGTCTAGCAGACGCCATATATTACT	372
339	CCAGCAGAGCTATACGCACTCAGCGCTTGGCATCTGAGGACTCTCGGCTCTATTACT	398
373	GTGCGCAAAATAGAGGGATATTTACTATGATTTTCACTTATGCCATGAGTACTGGGGTC	432
399	GTGCAAGAGAGGGGG-----TTACTCTGGTCCGACTATGCTTGGACTACTGGGGTC	452
433	AAGGAACCTCAGTCACCGTCTCCAGCAAAACAAACACCCCTCATGCTTATCCACTGG	492
453	AAGGAACCTCAGTCACCGTCTCCAGCAAAACAAACACCCCTCATGCTTATCCACTGG	512
493	CCCTGGGTGTGGAGATPACAACTGGTTCCTCCGTGACTCTGGGATGCTGGTCAAGGGCT	552
513	CCCTGGATCTGTGCCCAAACTAACTCCATGGTGACCTGGGATGCTGGTCAAGGGCT	572
553	ACTTCCCTGAGTCACTGAGTGTGACTGGTGAACCTGGTCCCTGTCAGCAGTGTGCACA	612
573	ATTTCCCTGAGCCAGTGCAGAGTGCAGTGAACCTGGATCCCTGTCAGCGGTGTGCACA	632
613	CTTCCAGCTCTCTGCACTGTGGACTTACACTATGAGCAGCTCAGTACTGTCCTCT	672
633	CTTCCAGCTCTCTGCACTGTGGACTTACACTATGAGCAGCTCAGTACTGTCCTCT	692
673	CCAGCAGCTGGCCAAAGTCAAGCTGACCGTCACTGACCGTTCCTACCCAGCCAGCAGCA	732
693	CCAGCCCTGGCCCAAGGAGAGCTGACCGTCACTGACCGTTCCTACCCAGCCAGCAGCA	752
733	CGGTGGCAAAAAAATCTGAGCCAGCGGGGCCATTTCAACAAATCAAGCCCTGCTCCAT	792
753	AGGTGGACAGAAATTTGTCGCCAGGGATTTGGTGTAGAGCTTGCATATG-----	804
793	GCAAGAGGTCTCAAAATGGCCAGCTCTCAACCTGAGGTGGAGTGCATCCGCTCTCATCT	852
805	-----TACAGTCCCAAGAGTATCATCTGCTTCATCT	836
853	TCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAGGTCAGCTGTGTGG	912
837	TCCTCCCAAAAGCCCAAGGATGTGTCTACCATTTACTCTGACTCTCAAGCTGCTGTG	896
913	TGCTGGATGTGAGCGAGGATGACCCAGACCTCCAGATCAGCTGTTGTGAACACCTGG	972
897	TGCTAGACATCAGCAAGGATGATCCCGAGTTCAGTTCAGTGGTTGTAGATGATGG	956
973	AAGTACACAGCTCAGACACAAACCCATAGAGAGGATTAACAACAGTACTATCCGGGTGG	1032

Search completed: June 23, 2003, 20:29:03
Job time : 416.773 secs

Db	957	AGGTGCACACAGCTCAGACGCAACCCCGGGAGGAGCAGTTCACAGCACTTTCCGCTCAG	1016
QY	1033	TCAGACACCTCCCATCCAGCAGCAGGACTGGATGAGTGGCAGAGTTCAAATGAAGG	1092
Db	1017	TCAGTGAATCTTCCCATCATGTCACCAAGGACTGGCTCAATGGCAAGGAGTTCAAATGCGGG	1076
QY	1093	TCAACAAACAAAGACCTCCCATCACCATCGAGAGAACCATCTCAAAAATTAAGAGGCTAG	1152
Db	1077	TCAACAGTGCAGCTTCCCTGCCCCATCGAGAAACCATCTTCCAAAACCAAGGCAGAC	1136
QY	1153	TCAGAGCTCCCAAGTATACATCTTTCGCCCCACAGCAGCAGTGTGCCAGGAAAGATG	1212
Db	1137	CGAAGGCTCCACAGTGTACACCATTCACCTCCCAAGGAGCAGATGGCCAAAGGATAAG	1196
QY	1213	TCAGTCTCACTTGGCTGGTGGGCTTCAACCCCTGGAGACATCACTGTGGAGTGGACA	1272
Db	1197	TCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTTACTGTGGAGTGGCAGT	1256
QY	1273	GCAATGGGCATACAGAGGAGGAGTACAGGACACCGCAGCTCCCTGGACTCTGACGTT	1332
Db	1257	GGAATGGGCAGCCGCGGAGAACTACAAGAACACTCAGCCCATCATGAACACAGATGGCT	1316
QY	1333	CTTACTTTCATATATAGCAAGCTCAATATGAAAAACAAGTGGGAGAAAAACAGATTCT	1392
Db	1317	CTTACTTCTCTACAGCAAGCTCAATGTGAGAGAGCAACTGGGAGGCGAGGAATACTT	1376
QY	1393	TCTCATGCAACGTGAGACACGAGGCTCTGAAAAATTTACTACCTGAGAGAGCCTCTCC	1452
Db	1377	TCAGCTGCTGTGTGTACATGAGGCTTGCACAACCCATACCTGAGAGAGCCTCTCC	1436
QY	1453	GGTCTCCGGTAAATGAGCTCAGCACCACAAAGCTCTCAGGTCTCTAAGAGACACTGGCA	1512
Db	1437	ACTCTCTGGTAAATGATCCAGTCTCTGGAGCCCTCTGGTCTCTACAGGACTCTGACA	1496
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Db	1497	CCTACTCCACCCCTCCC-TGTATAATAAAGCACCCAGCACTGCTCTTG	1544



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:26:36 ; Search time 4270.96 seconds
(without alignments)
10820.814 Million cell updates/sec

Title: US-09-770-916-1

Perfect score: 1588

Sequence: 1 ccattcttctcatagc.....taaaaaaaaaaaaaaaaaaaaa 1588

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*

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40: em.htgo_mus.*

41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1232.2	77.6	1616	10	BC010327	BC010327 Mus muscu
2	1195.8	75.3	1578	10	BC025447	BC025447 Mus muscu
3	1174.2	73.9	1579	10	MMIG6H	X13188 Mouse mRNA
4	1155.8	72.8	1546	10	MMTMIIGH	X67210 M.musculus
5	1093.8	68.9	1113	10	MMIG7	V00799 Mouse mRNA
6	1084	68.3	1389	6	AX466450	AX466450 Sequence
7	1083.4	68.2	1171	10	MUSIGHAK3	L00051 Mus musculu
8	1081.2	68.1	1365	6	AX466448	AX466448 Sequence
9	975	61.4	1653	10	BC018365	BC018365 Mus muscu
10	954.4	60.1	1564	10	BC019489	BC019489 Mus muscu
11	950	59.8	1594	10	BC012207	BC012207 Mus muscu
12	944.4	59.5	1620	10	BC003888	BC003888 Mus muscu
13	940.8	59.2	1570	6	A22261	A22261 M.musculus
14	940.8	59.2	1593	10	BC018535	BC018535 Mus muscu
15	939.2	59.1	1570	6	AR029102	AR029102 Sequence
16	937.6	59.0	1570	6	A77138	A77138 Sequence 6
17	933	58.8	1581	6	A78881	A78881 Sequence 1
18	933	58.8	1581	10	MMIGHC2AA	X70423 M.musculus
19	932	58.7	1658	10	BC031470	BC031470 Mus muscu
20	925.2	58.3	1584	10	BC003878	BC003878 Mus muscu
21	922.4	58.1	1573	10	BC018280	BC018280 Mus muscu
22	914.6	57.6	1568	6	E33134	E33134 Humanized a
23	889.6	56.0	1410	10	MMU421677	AJ421677 Mus muscu
24	885	55.7	7528	6	AX080953	AX080953 Sequence
25	883.6	55.6	1488	10	D17387	D17387 mRNA for mo
26	821.8	51.8	1095	10	MMIG6	V00798 Mouse mRNA
27	803.4	50.6	1341	6	I07390	I07390 Sequence 4
28	768.2	48.4	1431	6	AX055011	AX055011 Sequence
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34	737.8	46.5	6729	6	AX080954	AX080954 Sequence
35	734.4	46.2	990	10	MMU294738	AJ294738 Mus muscu
36	731.8	46.1	1523	10	BC008237	BC008237 Mus muscu
37	731.4	46.1	1643	10	BC024405	BC024405 Mus muscu
38	727.6	45.8	1558	10	AF466769	AF466769 Mus muscu
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40	720.4	45.4	1572	6	I64458	I64458 Sequence 23
41	715.2	45.0	1528	6	E00399	E00399 Mouse anti-
42	712.8	44.9	1542	10	BC002121	BC002121 Mus muscu
43	705.6	44.4	1505	10	KMAHCH	X87228 M.musculus
44	703.2	44.3	1517	10	MMU65534	U65534 Mus musculu
45	701.8	44.2	1557	10	BC003435	BC003435 Mus muscu

ALIGNMENTS

RESULT 1	BC010327	BC010327	1616 bp	mRNA	linear	ROD 07-AUG-2002
LOCUS	BC010327	Mus musculus, clone MGC:6533	IMAGE:2651776	mRNA	linear	complete cds.
DEFINITION	BC010327	Mus musculus, clone MGC:6533	IMAGE:2651776	mRNA	linear	complete cds.
ACCESSION	BC010327	Mus musculus, clone MGC:6533	IMAGE:2651776	mRNA	linear	complete cds.
VERSION	BC010327.1	GI:16307556				
KEYWORDS	MGC.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 (bases 1 to 1616)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-JUL-2001) National Institutes of Health, Mammalian					


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RESULT 3
MITE6H
JCUS
DEFINITION
Mouse mRNA for anti-hPLAP-directed immunoglobulin E6-H chain.
X13188
ACCESSION
X13188.1 GI:51780
KEYWORDS
Ig heavy chain; immunoglobulin.
SOURCE
Mus musculus.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1579)
De Waele, P., Feys, V., Van de Voorde, A., Molemans, F., and Fiers, W.
Expression in non-lymphoid cells of mouse recombinant
immunoglobulin directed against the tumour marker human placental
alkaline phosphatase
Eur. J. Biochem. 176 (2), 287-295 (1988)
JOURNAL
88329081
MEDLINE
3138116
PUBMED
Achieved expression in non lymphoid cells.
LOCATION/Qualifiers

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52..1479
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109..1476
mat_peptide
BASE COUNT 417 a 446 c 376 g 340 t
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Best Local Similarity 85.7%; Pred. No. 9.1e-306;
Matches 1334; Conservative 0; Mismatches 208; Indels 15; Gaps 2;
QY 16 AGAGCCTCCATCAGAGCATGGCTGCTTGGGGCTGCTCTTCTGCTGGTGACATTCGCCAA 75
Db 35 ACACACTGACTCAACCATGGAATGGATCTGATCTTCTCTTCTATCTCTGTCAGGAACGTG 94
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Db 95 CAGGTGTCCAATCCAGGTTCAAGTTCAGCTGACAGCTCTGGAGCTGAGCTGGCGAGGCTGGG 154
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RESULT 4

MMTVLIGH	1546 bp	mRNA	linear	ROD 07-AUG-1992
LOCUS				
DEFINITION	M.musculus rearranged immunoglobulin gamma 2b heavy chain.			
ACCESSION	X67210			
VERSION	X67210.1	GI:54826		
KEYWORDS	constant region; immunoglobulin; immunoglobulin heavy chain; variable region.			
SOURCE	Mus musculus.			
ORGANISM	Mus musculus			

REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Fischer.R.
TITLE	Direct Submission
JOURNAL	Submitted (06-JUL-1992) R. Fischer, Botanisches Inst. (BioI) der RWTH Aachen, Worringner Weg 1, 5100 Aachen, FRG
REFERENCE	2 (bases 1 to 1546)
AUTHORS	Fischer.R., Voss.A., Niersbach.M., Hunziker.W., Hirsch.H.J. and Kreuzaler,F.
TITLE	Production of a Tobacco mosaic virus (TMV) inactivating neotop
JOURNAL	Specific monoclonal antibody in Nicotiana tabacum
FEATURES	Unpublished
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Matches 1328; Conservative	0; Mismatches 197; Indels 24; Gaps 3;
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1081 ATAAAGCATCCAGCAAGCCTGGTACCATGTAA 1113

RESULT 6

AX466450
LOCUS AX466450 1389 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 3 from Patent WO0218443.
ACCESSION AX466450
VERSION AX466450.1 GI:21899963
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Esinger, D., Stiles, L., Lamarque, A. and Jelinek, T.
TITLE A recombinant monoclonal antibody to phosphotyrosine-containing proteins
JOURNAL Patent: WO 0218443-A 3 07-MAR-2002;
UPSTATE BIOTECHNOLOGY, INC. (US)
FEATURES
Location/Qualifiers
1..1389
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cDNA for heavy chain of recombinant antibody with 3'-histidine tag sequence"
BASE COUNT 369 a 395 c 335 g 289 t 1 others
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Query Match 68.3%; Score 1084; DB 6; Length 1389;
Best Local Similarity 87.2%; Pred. No. 2.1e-281;
Matches 1218; Conservative 1; Mismatches 156; Indels 21; Gaps 2;
QY 91 AGGTGACGCTGAAGCAGTCAGGACCTGGCTAGTGCAGCCCTCACAGAGCCCTGCATCA 150
Db 2 AGGTGACGCTGAAGCAGTCAGGACCTGGCTAGTGCAGCCCTCACAGAGCCCTGCATCA 61
QY 151 CCGTGCACAGTCTCTGGTTCTCTCAATTAAGTATGCTGATACATGGGTTCCTGATCTC 210
Db 62 CCGTGCACAGTCTCTGGTTCTCTCAATTAAGTATGCTGATACATGGGTTCCTGATCTC 121
QY 211 CAGGAAAGGCTTGGAGTGGCTGGAGTGTATGAGT---GGTGGAGACACAGACTATA 267
Db 122 ATGGAGAGAGCCCTTGGTGGATTTGAGGTATTAATCTTACTATGTTGGTGTCTATCTCA 181
QY 268 ATGACGCTTTTATATCCAGACTGACATCAGCAAGAGCAATTCAGAGCCCACTCTCT 327
Db 182 GCGCGAAGTTCAAGGCAAGGCCAATTTGACTGTAGACAAGTCTCCAGCAGCAGCTACA 241
QY 328 TTAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCGAGAAATAGAG 387
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QY 388 GGGATATTACTATGATTTCACTTATGCCATGAGTACTGGGGTCAAGGAACCTCAGTCA 447
Db 302 GGG-----CGTACTTGTACTTGGGGCAAGGCCACCTCTCA 343
QY 448 CCGTCTCTCAGCCAAAACACACCCCATCAGTCTATCTATCCAGTGGCCCTGGGTGTGAG 507
Db 344 CAGTCTCTCAGCCAAAACACACCCCATCAGTCTATCCAGTGGCCCTGGGTGTGAG 403
QY 508 ATACAAGTGTCTCTCCGCTGACTCTGCGATGCTGCGTCAAGGGCTACTTCCCTGAGTCA 567
Db 404 ATACAAGTGTCTCTCCGCTGACTCTGCGATGCTGCGTCAAGGGCTACTTCCCTGAGTCA 463
QY 568 TGACTGTGACTTTGGAACCTCTGGATCCCTGCTCCAGCAGTGTGCACACCTTCCAGCTCTCC 627
Db 464 TGACTGTGACTTTGGAACCTCTGGATCCCTGCTCCAGCAGTGTGCACACCTTCCAGCTCTCC 523
QY 628 TGCAGTCTGAGTCTTACACTATGAGCAGTCTGAGTCTGCTCCCTCCAGCAGCTGGCCAA 687
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742 CCCACCCGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 798

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919 GCGCATGTGACATGT 978

952 GCTGGTGTGACACAGTGTGACATGTGACATGTGACATGTGACATGTGACATGTGAC 1011

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1279 AAATGTGTGTGAGTGTGACAGGAAAGATGTGACAGTGTGACAGTGTGACAGTGTGAC 1338

1312 CAGTCTGAGTGTGAGTGTGACAGGAAAGATGTGACAGTGTGACAGTGTGACAGTGTGAC 1371

1339 CAGTCTGAGTGTGAGTGTGACAGGAAAGATGTGACAGTGTGACAGTGTGACAGTGTGAC 1398

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1399 CTGGGAGAAAGAGAGTCTTTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1458

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QY I552 CAAAGCTGTACCATGTAAAAA 1588

Db I579 CAAAGCTGGACCATGTAAAAA 1615

RESULT 10

BC019489

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC019489 1564 bp mRNA linear ROD 07-AUG-2002

Mus musculus, Similar to immunoglobulin heavy chain 1 (serum

IgG2a), clone MGC:18984 IMAGE:4011654, mRNA, complete cds.

BC019489

BC019489.1 GI:18043008

MGC.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1564)

Strausberg, R.

Direct Submission

Submitted (19-DEC-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,

Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,

Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 23 Row: 6 Column: 23

This clone was selected for full length sequencing because it

passed the following selection criteria: Similarity but not

identity to protein.

Location/Qualifiers

1. .1564

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/db_xref="taxon:10090"

/map="C2ECH II"

/clone="MGC:18984 IMAGE:4011654"

/tissue_type="Mammary tumor metastasized to lung.

MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR

enhancer."

/clone_lib="NCI CGAP_Lu30"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

26. .1444

/codon_start=1

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IgG2a)"

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FEATURES

source

CDS

[illegible]

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956 CACACAGCTCAGACACAACCCATAGAGAGGATTACACAGTACTATCCGGGTGGTCAGT 1015
1038 ACCCTCCCATCCAGACACAGGACTGGATGAGTGGCAAGGAGTTCAATGCCAAGGTCAAC 1097
1016 GCCCTCCCATCCAGACACAGGACTGGATGAGTGGCAAGGAGTTCAATGCCAAGGTCAAC 1075
1098 AACAAAGACCTCCATCACCCTCGAGAGAACCATCTCAAAAATTTAAAGGGCTAGTCAGA 1157
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1278 GGGCATACAGAGAGACTACAGGACACCGCACCAGTCTCGGACTCTGACGGTTCTTAC 1337
1256 GGGAAAACAGAGCTAAACTACAAGAACACTGAACCACTCCTGGACTCTGATGGTTCTTAC 1315
1338 TTCATATATAGCAAGCTCAATATCAAAACAAAGCAAGTGGGAGAAACAGATTCCTTCTCA 1397
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DB 125 FAWGQGLTVTSAAKTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEVTVTWSGSL 184
QY 189 SSSVHTFPALLOGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKKLESPGISTI 248
DB 185 SSGVHTFPALLOGLYTLSSSVTVTSNTWPSQITCNVAHPASSTVDKKLEPRVPI-TQ 243
QY 249 NPCPPCKECHKCAPNLEGGPSVFIPPNKIDVLMISLTPKVTCCVVVDVSEDDPDVOISW 308
DB 244 NPCPPLKECPPCAAPDLGGPSVFIFPPKIKDVLMSLSPMVTCCVVVDVSEDDPDVOISW 303
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DB 304 FVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMGSKGFEKCKVNNKDLPSPIRTIS 363
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DB 364 KPGPVRAPQVYVLPPEAEEMTKKESLCTWITGFLPAEIAVDWTSNGRTEQNKNTATV 423
QY 429 LQSDGSFYIYSKLNMTSKWEKTSFSCNVRHGLKNYLLKKTISRSPGK 478
DB 424 LQSDGSFYMSKLRVQKSTWERSLFACSVHGLHNLTKTISRSLGK 473

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ID Q99L25 AC Q99L25;
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DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1;
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 473 AA; 5249 MW; BE9889B7986DA155 CRC64;

Query Match 67.4%; Score 1719.5; DB 11; Length 473;
Best Local Similarity 68.6%; Pred. No. 3.2e-133;
Matches 326; Conservative 58; Mismatches 80; Indels 11; Gaps 6;

QY 6 LFLCLVTFPSCVLQKQSGVLQKQSGVLSITCTVSGFSLTSYGVHWRQSPGKGLE 65
DB 8 LFLFSVT--TGVSQVQLQKQSGVLSITCTVSGFSLTSYGVHWRQSPGKGLE 65
QY 66 WLGVIW--SGGDTDYNAAFISRLSISKNSKQLFPKMSLRATDTAIYICARNRDIYD 124
DB 66 WIGYIYPRDGSRTYNEKFKGKATLTADKSSSTAYMQLNLTSEDSAVCFCSRQ-GSIYYG 124
QY 125 F-TYAMDYWGQCTSVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPEVTVTW 193
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QY 244 PISTINPCPPCKECHKCAPNLEGGPSVFIFPPNKKIDVLMISLTPKVTCCVVVDVSEDDPD 303
DB 245 P--TIKCPCC---KCPAPNLLGGPSVFIFPPKIKDVLMSLSPMVTCCVVVDVSEDDPD 298
QY 304 VQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMGSKGFEKCKVNNKDLPSPI 363
DB 299 VQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMGSKGFEKCKVNNKDLPSPI 358
QY 364 ERISIKLGLVRAPOVYILPPPAQOLSRKDVSLTCLVVGNGPDISVETWSNGHTEENYK 423
DB 359 ERISIKPKGSRAPQVYVLPPEAEEMTKKQVLTCTWYTFDMPEDYVETWSNGHTEENYK 418
QY 424 DTAPVLDSDGSFYIYSKLNMTSKWEKTSFSCNVRHGLKNYLLKKTISRSPGK 478
DB 419 NTEPVLSDSDGSFYMSKLRVQKSTWERSLFACSVHGLHNLTKTISRSPGK 473

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ID Q99L31 AC Q99L31;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1;
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 66.7%; Score 1703; DB 11; Length 468;
Best Local Similarity 68.1%; Pred. No. 7.1e-132;
Matches 324; Conservative 58; Mismatches 78; Indels 16; Gaps 6;

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DB 6 VIFFLMAVVGIVNSEQVQLQKQSGVLSITCTVSGFSLTSYGVHWRQSPGKGLE 65
QY 66 WLGVIW--SGGDTDYNAAFISRLSISKNSKQLFPKMSLRATDTAIYICARNRDIY 122
DB 66 WIG--WIDPEDGETYKAPKFDKATITADTSSNTAYLQLSLSLSEDTAIYICARN--LL 120
QY 123 YDTYAMDYWGQCTSVTVSSAKTTPSPVYPLAPCGDGTGSSVTLGCLVKGYFPEVTVT 182
DB 121 YGYIY--DYWGQCTTVTVSSAKTTPSPVYPLAPVCGDGTGSSVTLGCLVKGYFPEVTVT 178
QY 183 WNSGSLSSVHTFPALLOGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDKKLEPS 242
DB 179 WNSGSLSSVHTFPALLOGLYTMSSSVTVPSSTWPSQITCNVAHPASSTVDKKLEPR 238
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[illegible]

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ID
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AC
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DT 01-JUN-2001 (TtEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TtEMBLrel. 21, Last annotation update)
DE Similar to RIKEN cDNA l810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
OX
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
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RESULT 8	
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ID	Q9R

Q9R1A4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
IGH-4.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RW "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
ST EMBL; AF152372; AAD40243.1; -;
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003600; Igh-like.
DR InterPro; IPR003006; Igh-MHC.
DR InterPro; IPR003596; Igh-V.
DR Pfam; PF00047; Igh-4.
DR SMART; SM00406; Igh; 1.
DR SMART; SM00410; Igh-like; 2.
DR PROSITE; PS00290; IGH_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
FT SEQUENCE 437 AA; 48142 MW; 5C3A7B3EE7D697C CRC64;
Query Match 57.1%; Score 1456.5; DB 11; Length 437;
Best Local Similarity 61.1%; Pred. No. 1.3e-111;
Matches 280; Conservative 62; Mismatches 95; Indels 21; Gaps 7;
QY 21 VOLKSGELVLPQSLSITCTVSGFSLTSYGVHVRQSPGKLEWLGVWISGGTDYNA 80
DB 1 VOLKSGGLVLPKGSGLKLSAASGFTSSYAMSWVRQTPKRLLEWASFSGGIYYTD 60
QY 81 AFISRLSISKDNKSOLFKNLSLRATDTAIYCARNRGDIYDFTYANDYWGQTSVTV 140
DB 61 SVKGRTIYKDKRNLISLQSSLSRSEDYAYCA--RGD-----YSA-YGPGTIVTV 111
QY 141 SAKTTPSVPLAPGCGDGTGSSVTLGLVKGYPPESVTVTWNSGSLSSSVHTFPALLO 200
DB 112 SAAKTPPSVPLAPGSAQAATNSMTLGLVKGYFPEPTVTVWNSGSLSSGVHTFPALV 171
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DB 223 TVPEVS---SVFIIPPCKPDLVTLITLTKVTCVVVDISKDDPEVQFSWFDVDEHTAQT 279
QY 321 QTHREDYNSITRVSTLPIQHDWMSGKEFKVKVKNKDLPSPIERTISKIGLVRAPOVY 380
DB 280 QPREQFNSTRSVSELPIMHQDLWNGEKKRVNSAAPPAPIEKTIKTKGRAPQVY 339
QY 381 ILPPPAEQLSRDYSLATLVGVNFGDISVEVTSNGHTEENYKDTAPVLDSDGSIYISK 440
DB 340 TIPPPEQMAKDKVSLTCMTIDFFEDITVEQWNGQPAENYKNTQPIMDTDGSIYISK 399
QY 441 LNMKTSKWEKTDSPCNVRHGLKNYLLKKTISRSPGK 478
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RESULT 9

Q8TC77

ID Q8TC77

PRELIMINARY;

PRT; 471 AA.

Q8TC77;

01-JUN-2002 (TrEMBLrel. 21, Created)

01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothenical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC024289; AAH24289.1; -;
KW Hypothenical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
Query Match 55.2%; Score 1409; DB 4; Length 471;
Best Local Similarity 57.3%; Pred. No. 1.2e-107;
Matches 275; Conservative 74; Mismatches 115; Indels 16; Gaps 7;
QY 4 LGLLFC-LVTFPSCVLSQVOLKSGPGLVQPSQSLSTCTVSGFSLTSYGVHVRQSPGK 62
DB 3 LGLRWVFLVAILEGVQCEQVLESGLVKPGSLRLSCAASGFTSSYSMNVVRQAPGK 62
QY 63 GLEWLGIVISGGTDYNAFI-SRLSISKDNKSOLFKNLSLRATDTAIYCARNRGDI 121
DB 63 GLEWVSSMSSSSYIYADSVKGRFTISRDNKNSLYLQMNLSLRAEDTAVYYCARDLRQL 122
QY 122 --YDFTYANDYWGQTSVTVSSAKTTPPSVYPLAPCCGDTTGSSTVTLGLVKGYPPESV 179
DB 123 TSYWYF----DLWGRGTLTVTVSSASTKGPSPVFLAPSSKTSGGTAALGCLVKDYFPEV 178
QY 180 TVTWNSGSLSSSVHTFPALLO-SGLYTMSSSVTVPSSTWPSQVTCVAHPASSTVDK 238
DB 179 TVSWNSGALTSGVHTFPALVLOSSLGLSLSSVTVPSSSLGTQYICNVNKHKPNKTKVDK 238
QY 239 LEFSGPISTINCPCKECHKC PAPNLEGGPSVFIIPPNIKDVLMISLTTPKVTGVVDV 298
DB 239 VEPKSCDKT-HTCPP-----CPAPELLGSPSVLEFPKPKDTLMISRTPEVTCVVVDV 291
QY 299 EDDPDVQISWVFNVEHTAQTQTHREDYNSITRVSTLPIQHDWMSGKEFKCKVKNKD 358
DB 292 HDPEYKFNWYDGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 351
QY 359 LPSPERTISKIGLVRAPOVYILPPAEQLSRDYSLATLVGVNFGDISVEVTSNGHT 418
DB 352 LPAPIEKTIKTKGRAPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 411
QY 419 EENYKDTAPVLDSDGSIYFIYSKINMKTISKWEKTDSPCNVRHGLKNYLLKKTISRSPGK 478
DB 412 ENNYKTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
RESULT 10
Q8TC63
ID Q8TC63
PRELIMINARY; PRT; 473 AA.
Q8TC63;
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothenical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -;
KW Hypothenical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

QY	237	KKLEPSPGISTIN-PCPP-CKECHKCAPNLEGSPVFI	PPPNIKDVLMSLTPKVTGV	294
Db	236	---DSNPVOELNVCNCGICSPPTTPPPSCQ--PSLSLRPALEDLLGS-DASITCTL	278	
QY	295	VDSEDDPDVOISVNNVNVHTAQTTHREDYNSI--IRVVSTLPIQHODMWSCKEFK	351	
Db	279	NGLRDPGAV-FTW-----EPSTGKDQAVOKKAVONGSCGYSSVSLPGCAERNWSGASF	332	
QY	352	CKVNNKDLPSPIERTISKIGLVRAPQVYILPPAPQLSRKD-VSLTCLVWGFNPGDISV	410	
Db	333	CTVTHPE-SDTLGCTAKVTNTFPQVHLLPPPSSEELALNELVSLTCLVRAFNPKVELV	391	
QY	411	EWTSGHTE---ENYKDTAPVLD-SDG--SYFIYSKLNKMTSKWEKTDTSFSCNVRHEGLK	464	
Db	392	RWL-HGNEELSPESYLVEFLKPEPGEGATYLVTSVLVRSATLWQGDQDOYSCWVGHEALP	450	
QY	465	NYLKKTIISRPCK	478	
Db	451	MNFQTKIDRLSGK	464	
RESULT 13				
QY	921K1	PRELIMINARY;	PRT;	278 AA.
Db	Q921K1			
QY	01-DEC-2001	(T-EMBLrel. 19, Created)		
Db	01-DEC-2001	(T-EMBLrel. 19, Last sequence update)		
QY	01-MAR-2002	(T-EMBLrel. 20, Last annotation update)		
Db	Unknown	(protein for MGC:18977).		
QY	Unknown	(protein for MGC:18977).		
Db	Unknown	(protein for MGC:18977).		
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QY	Unknown	(protein for MGC:18977).		

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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:52 ; Search time 19.4691 Seconds
(without alignments)
1018.315 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLFLCLVFPSCVLSQ.....RHGLKNYLLKTKTSRSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	70.6	336	1	GCB_MOUSE
2	1797	70.4	405	1	GCBM_MOUSE
3	1419	55.6	330	1	GCAA_MOUSE
4	1414	55.4	399	1	GCAAB_MOUSE
5	1385.5	54.3	335	1	GCAAB_MOUSE
6	1326.5	52.0	333	1	GCB_RAT
7	1202.5	47.1	329	1	GCC_RAT
8	1170	45.8	329	1	GC3_MOUSE
9	1159	45.4	398	1	GC3_MOUSE
10	1150	45.1	324	1	GC1_MOUSE
11	1145	44.9	393	1	GC1M_MOUSE
12	1112	43.6	326	1	GC1_MOUSE
13	1100	43.1	322	1	GCA_RAT
14	1087	42.6	330	1	GC1_HUMAN
15	1080.5	42.3	323	1	GC_RABIT
16	1080.5	42.3	329	1	GC2_CAVPO
17	1059	41.5	326	1	GC2_HUMAN
18	1054.5	41.3	327	1	GC4_HUMAN
19	777.5	30.5	290	1	GC3_HUMAN
20	584	22.9	116	1	HV45_MOUSE
21	556	21.8	144	1	HV43_MOUSE
22	502	19.7	115	1	HV44_MOUSE
23	478	18.7	454	1	MDC_HUMAN
24	477.5	18.7	429	1	EPC_RAT
25	474	18.6	421	1	EPC_MOUSE
26	473	18.5	428	1	EPC_HUMAN
27	442.5	17.3	438	1	HVC2_HETFR
28	437.5	17.1	370	1	HVC1_HETFR
29	435.5	17.1	438	1	HVC3_HETFR
30	432.5	16.9	458	1	MDC_RABIT
31	429	16.8	391	1	MOCB_HUMAN
32	426.5	16.7	393	1	HVC3_HETFR
33	425.5	16.7	461	1	HVCM_HETFR

34 422.5 16.6 479 1 MUCM_RABIT
35 420 16.5 450 1 MUC_CANFA
36 417 16.3 457 1 MUC_SUNMU
37 402.5 15.8 353 1 ALCI_GORGO
38 397 15.6 135 1 HV02_XENLA
39 387 15.2 340 1 ALC2_HUMAN
40 383.5 15.0 137 1 HV46_MOUSE
41 383.5 15.0 353 1 ALC1_HUMAN
42 380 14.9 344 1 ALC_MOUSE
43 372.5 14.6 454 1 MUC_MESAU
44 372.5 14.6 455 1 MUC_MOUSE
45 362.5 14.2 476 1 MUCM_MOUSE

ALIGNMENTS

RESULT 1
GCB_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2B chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (A ALLELE).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=80081502; PubMed=117549;
RA Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
RT "Sequence of the cloned gene for the constant region of murine gamma
2b immunoglobulin heavy chain.";
RL Science 206:1303-1306(1979).
RN [4]
RP SEQUENCE FROM N.A. (B ALLELE).
RX MEDLINE=82173203; PubMed=6803173;
RA Ollio R., Rougeon F.;
RT "Mouse immunoglobulin allotypes: post-duplication divergence of gamma
2a and gamma 2b chain genes.";
RL Nature 296:761-763(1982).
RN [5]
RP CARBOHYDRATE-LINKAGE SITE THR-105.
RX MEDLINE=94216359; PubMed=7512967;
RA Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimura T., Takahashi N., Kato K., Arata Y.;
RT "O-glycosylation in hinge region of mouse immunoglobulin G2b.";
RL J. Biol. Chem. 269:12345-12350(1994).
CC -I- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
MODIFIED WITH 2 SIALIC ACID RESIDUES.
CC -I- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA
CHAINS.
CC -I- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.
DR PIR; A02157; G2MS11.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.

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InterPro: IPR003600; Ig_Like.  
Pfam: PF00047; Ig_3.  
SMART: SM00410; Ig_Like; 1.  
SMART: SM00407; IG1; 2.  
PROSITE: PS00290; IG_MHC; 1.  
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
NON_TER 1  
DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
DISULFID 27 82  
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 150 210  
DISULFID 256 314  
CARBOHYD 105 105 O-LINKED (GALNAc...).  
MOD_RES 336 336 REMOVED POST-TRANSLATIONALLY (PROBABLE).  
VARIANT 163 163 Q -> R (IN B ALLELE).  
VARIANT 194 194 T -> A (IN B ALLELE).  
VARIANT 300 300 M -> D (IN B ALLELE).  
VARIANT 301 301 M -> I (IN B ALLELE).  
CONFLICT 25 25 L -> S (IN REF. 2 AND 3).  
CONFLICT 36 36 S -> P (IN REF. 2 AND 3).  
CONFLICT 239 239 I -> T (IN REF. 2 AND 3).  
SEQUENCE 336 AA; 36658 MW; 7D879662607C356E CRC64;  
Query Match 70.6%; Score 1802; DB 1; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.2e-120; Indels 0; Gaps 0;  
Matches 336; Conservative 0; Mismatches 0;  
143 AKTTPSVYPLAPGCGDTGSSVTGCLVKGYFPESVTVTWNSGSLSSSVHFFPALQSG 202  
|||||  
1 AKTTPSVYPLAPGCGDTGSSVTGCLVKGYFPESVTVTWNSGSLSSSVHFFPALQSG 60  
203 LYTMSSSVTPSPSTWPSQTVCVAHPASSTVDDKLEPSGPISTINPCPCKECHKCPA 262  
|||||  
61 LYTMSSSVTPSPSTWPSQTVCVAHPASSTVDDKLEPSGPISTINPCPCKECHKCPA 120  
263 PNLGGPSVFIIPPNIKDVLMISLTPKVTVCVVVDSEDDPDVQISWFWNNVEVHTAQOT 322  
|||||  
121 PNLGGPSVFIIPPNIKDVLMISLTPKVTVCVVVDSEDDPDVQISWFWNNVEVHTAQOT 180  
|||||  
323 HREDNSTIRVSTLPIQHDQMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYL 382  
|||||  
181 HREDNSTIRVSTLPIQHDQMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYL 240  
|||||  
383 PPPAQQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442  
|||||  
241 PPPAQQLSRKDVSLTCLVVGFPNGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300  
443 MKTSKWKETDSCFNVRHGLKNYLLKTTISRSPG 478  
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301 MKTSKWKETDSCFNVRHGLKNYLLKTTISRSPG 336  
|||||  
RESULT 2  
GBM_MOUSE STANDARD; PRT; 405 AA.  
P01867:  
21-JUL-1986 (Rel. 01, Created)  
01-AUG-1991 (Rel. 19, Last sequence update)  
15-JUL-1999 (Rel. 38, Last annotation update)  
Ig gamma-2B chain C region, membrane-bound form.  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI_TaxID=10090;  
[1]  
SEQUENCE OF 335-405 FROM N.A.  
MEDLINE=82222190; PubMed=6283537;  
Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;  
"Nucleotide sequences of gene segments encoding membrane domains of  
immunoglobulin gamma chains.";
```

```
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
[2]  
SEQUENCE OF 335-378 FROM N.A.  
MEDLINE=82115295; PubMed=6799207;  
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
Eisenberg D., Wall R.;  
"Gene segments encoding transmembrane carboxyl termini of  
immunoglobulin gamma chains.";  
Cell 26:19-27(1981).  
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
BOUND CHAINS. IN THAT IT CONTAINS AN ALTERNATIVE 3' END. ENCODED  
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
SEGMENT OF MU CHAINS.  
-!- MISCELLANEOUS: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA  
CHAINS.  
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE  
IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.  
-!- MISCELLANEOUS: THE A ALLELE SEQUENCE IS SHOWN.  
-----  
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-----  
EMBL: J00462; AAB59659.1; ALT_INIT.  
PIR: C02154; G2MSBM.  
HSP: P01842; 7FAB.  
MGD: MGI:96445; Igh-3.  
InterPro: IPR003006; Ig_MHC.  
InterPro: IPR003597; Ig-CL.  
InterPro: IPR003600; Ig_Like.  
Pfam: PF00047; Ig_3.  
SMART: SM00410; Ig_Like; 1.  
SMART: SM00407; IG1; 2.  
PROSITE: PS00290; IG_MHC; 1.  
Immunoglobulin domain; Immunoglobulin C region; Transmembrane;  
Alternative splicing.  
NON_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).  
DISULFID 15 15  
DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).  
DISULFID 150 210  
DISULFID 256 314  
DISULFID 256 314  
TRANSMEM 352 369  
DOMAIN 370 405 POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;  
Query Match 70.4%; Score 1797; DB 1; Length 405;  
Best Local Similarity 100.0%; Pred. No. 3.6e-120; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 0;  
QY 143 AKTTPSVYPLAPGCGDTGSSVTGCLVKGYFPESVTVTWNSGSLSSSVHFFPALQSG 202  
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Db 1 AKTTPSVYPLAPGCGDTGSSVTGCLVKGYFPESVTVTWNSGSLSSSVHFFPALQSG 60  
QY 203 LYTMSSSVTPSPSTWPSQTVCVAHPASSTVDDKLEPSGPISTINPCPCKECHKCPA 262  
|||||  
Db 61 LYTMSSSVTPSPSTWPSQTVCVAHPASSTVDDKLEPSGPISTINPCPCKECHKCPA 120  
QY 263 PNLGGPSVFIIPPNIKDVLMISLTPKVTVCVVVDSEDDPDVQISWFWNNVEVHTAQOT 322  
|||||  
Db 121 PNLGGPSVFIIPPNIKDVLMISLTPKVTVCVVVDSEDDPDVQISWFWNNVEVHTAQOT 180  
QY 323 HREDNSTIRVSTLPIQHDQMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVYL 382  
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Db 181 HREDYNSTIRVVSTLPQHDMWNGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
QY 383 PPPAEQLSRKDVSLCLVGVNPGDISVETWNGHTEENYKDTAPVLDSDGSFYFYISKLN 442
Db 241 PPPAEQLSRKDVSLCLVGVNPGDISVETWNGHTEENYKDTAPVLDSDGSFYFYISKLN 300
QY 443 MKTSKWKTDSPSCNVRHGLKNYLYKTKTISRSPG 477
Db 301 MKTSKWKTDSPSCNVRHGLKNYLYKTKTISRSPG 335
RESULT 3
SCAA_MOUSE
ID GCAM_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=81076554; PubMed=6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
[2]
SEQUENCE FROM N.A.
MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
and evolution of heavy chain genes: further evidence for intervening
sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
[3]
SEQUENCE FROM N.A.
MEDLINE=81223894; PubMed=6787604;
Ollio R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
suggests that exons can be exchanged between genes in a multigenic
family.";
Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
[4]
MYELOMA PROTEIN MOPC 173.
MEDLINE=74175517; PubMed=4831970;
Bourgeois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a
immunoglobulin: amino-acid sequence of the FC fragment. Implications
for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
[5]
DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2a
immunoglobulin. Identification of the disulfide bridges.";
Eur. J. Biochem. 30:452-462(1972).

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; V00798; CAA24178.1; --
PIR; A02152; G2MSA.
HSP; P01842; 7FAB.

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; ig; 2; like.
DR SMART: SM00410; Ig_like; 1.
DR SMART: SM00407; Igcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
Query Match 55.6%; Score 1419; DB 1; Length 330;
Best Local Similarity 78.6%; Pred. No. 1.6e-93;
Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;
QY 143 AKTTPSVVYPLAPGGGDTGSSVTLGLVKGYPESVTVTNWSSGSLSSSVHTFPALQSG 202
Db 1 AKTTPSVVYPLAPVCGDGTGSSVTLGLVKGYPPEVTVTNWSSGSLSSGVHTFPVQLSD 60
QY 203 LYTMSSSVTPSSTWPSQTCVAHPASSTVVDKLEPGSPITINPCPKCKECHKCPA 262
Db 61 LYTLSSSVTVSTWPSQITCNVAHPASSTVKDKIEPRGP--TIKPPC---KCPA 114
QY 263 PNLGGPSVFIIPPNIKDVLMISLTPKVTVVVDVSEDDPDVQISWVNVVHTAQTOT 322
Db 115 PNLGGPSVFIIPPNIKDVLMISLTPKVTVVVDVSEDDPDVQISWVNVVHTAQTOT 174
QY 323 HREDYNSTIRVVSTLPQHDMWNGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
Db 175 HREDYNSTIRVVSTLPQHDMWNGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 234
QY 383 PPPAEQLSRKDVSLCLVGVNPGDISVETWNGHTEENYKDTAPVLDSDGSFYFYISKLN 442
Db 235 PPPEEMTKQVTLTCMVTFDMPEDIYVETWNGKTELNYKNTPEVLDSDGSFYFYISKLR 294
QY 443 MKTSKWKTDSPSCNVRHGLKNYLYKTKTISRSPG 478
Db 295 VEKKNWVERNSYSCSVVHGLHNHHTKSFSTPGK 330
RESULT 4
GCAM_MOUSE
ID GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.

!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF THE A ALLELE.

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EMBL; J00471; AAB59661.1; ALT_INIT.

PIR; A02154; G2MSAB.

HSSP; P01842; 7FAB.

MGI; 96443; Igh-1.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003600; Ig_Like.

Pfam; PF00047; Ig; 2.

SMART; SM00410; Ig_Like; 1.

SMART; SM00407; Ig_C1; 2.

PROSITE; PS00290; Ig_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

Transmembrane; Alternative splicing.

NON_TER 1

DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

DISULFID 144 204

DISULFID 250 308

DISULFID 346 363

DOMAIN 364 399

CARBOHYD 180 180

SEQUENCE 399 AA; 44020 MW; 4C3813BFAED3FF0 CRC64;

Query Match 55.4%; Score 1414; DB 1; Length 399;

Best Local Similarity 78.5%; Pred. No. 4.7e-93;

Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

143 AKTTPSVVPLAPCGDITGSSVTLGCLVKGYEPESVTVTNWSSLSVSSVHTFPALQSG 202

1 AKTAPSVVPLAPVCGDITGSSVTLGCLVKGYEPPEVTLTNWSSLSVSSVHTFPALQSD 60

203 LYTMSSSVTPSPSTWPSQVTCVAHPASSTVVDKKEPSPSTINPCPPCKECKCPA 262

61 LYTSSSVTVSTWPSQVTCVAHPASSTVVDKKEPSPSTINPCPPCKECKCPA 114

263 PNLEGGPSVFIFPPNKKVLMISLTPKVCVVVDSEDDPDVQISWVNNVEVHTAQQT 322

115 PNLLGGPSVFIFPPNKKVLMISLTPKVCVVVDSEDDPDVQISWVNNVEVHTAQQT 174

323 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYL 382

175 HREDYNSTLRVWSALPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYL 234

383 PPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGVSFYISKLN 442

235 PPPAEEMTKQVLTCTCMVDFDPEYVETNNGKTELYKNTPELDSGVSFYISKLN 294

443 MKTSKWEKTDSPSCNVRHGLKNYLLKTTISRSPG 477

295 VEKNWVNSYSCSVVHGLNHHHTTKFSRTPG 329

RESULT 5

CAB_MOUSE

D GCAB_MOUSE

C P01864;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.

Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

PC STRAIN=C57BL/6;

RX MEDLINE=82037861; PubMed=6170065;

RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;

RT "Multiple differences between the nucleic acid sequences of the

IgG2a and IgG2b alleles of the mouse."

RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).

RN [2]

SEQUENCE.

RP MEDLINE=82037777; PubMed=6794027;

RA Dognin M.J., Lauwereys M., Strosberg A.D.;

RT "Multiple amino acid substitutions between murine gamma 2a heavy

chain Fc regions of Igla and Ig1b allotypic forms."

RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).

CC !- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,

FROM BALB/C MICE, AT 15% OF THE POSITIONS.

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EMBL; J00479; -; NOT_ANNOTATED_CDS.

PIR; A02153; G2MSAB.

HSSP; P01842; 7FAB.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003597; Ig_C1.

InterPro; IPR003600; Ig_Like.

Pfam; PF00047; Ig; 3.

SMART; SM00410; Ig_Like; 1.

SMART; SM00407; Ig_C1; 2.

PROSITE; PS00290; Ig_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region.

NON_TER 1

SEQUENCE 335 AA; 36596 MW; FA3382792CBBL3C6 CRC64;

Query Match 54.3%; Score 1385.5; DB 1; Length 335;

Best Local Similarity 77.1%; Pred. No. 3.9e-91;

Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

143 AKTTPSVVPLAPCGDITGSSVTLGCLVKGYEPESVTVTNWSSLSVSSVHTFPALQSG 202

1 AKTAPSVVPLAPVCGDITGSSVTLGCLVKGYEPPEVTLTNWSSLSVSSVHTFPALQSG 60

203 LYTMSSSVTPSPSTWPSQVTCVAHPASSTVVDKKEPSPSTINPCPPCKECKCPA 262

61 LYTSSSVTVSTWPSQVTCVAHPASSTVVDKKEPSPSTINPCPPCKECKCPA 119

263 PNLEGGPSVFIFPPNKKVLMISLTPKVCVVVDSEDDPDVQISWVNNVEVHTAQQT 322

120 PDLGGPSVFIFPPNKKVLMISLTPKVCVVVDSEDDPDVQISWVNNVEVHTAQQT 179

323 HREDYNSTIRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYL 382

180 HREDYNSTLRVWSALPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYL 239

383 PPPAEQLSRKDVSLTCLVGFNPGDISVETNSGHTENYKDTAPVLDSGVSFYISKLN 442

240 PPPAEEMTKQVLTCTCMVDFDPEYVETNNGKTELYKNTPELDSGVSFYISKLN 299

443 MKTSKWEKTDSPSCNVRHGLKNYLLKTTISRSPG 478

300 VQKSWERGLSFACSVVHGLNHHHTTKTISRSLGK 335


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FT FT DOMAIN 113 219 CH2.
FT FT DOMAIN 220 326 CH3.
FT FT DISULFID 27 82
FT FT DISULFID 102 102
FT FT DISULFID 106 106
FT FT DISULFID 109 109
FT FT DISULFID 111 111
FT FT DISULFID 140 200
FT FT DISULFID 246 304
FT FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 43.6%; Score 1112; DB 1; Length 326;
Best Local Similarity 61.9%; Pred. No. 8.8e-72;
Matches 208; Conservative 50; Mismatches 68; Indels 10; Gaps 3;

143 AKTTPPSVYPLAPCGDITGSSVTLGCLVKGYFPEPVTVVWNSGSLSSVHTFPAVLQSG 202
1 AETTAPSYIPLAPGTALKSNMVTGLGCLVKGYFPEPVTVVWNSGSLSSVHTFPAVLQSG 60
203 LYTMSSSVTPSSWPSQTVTCVAHPASSTVDKLLKLEPSGPISTINCPCKECKHCPA 262
61 LYTLTSSVTPSSWPSQTVTCVAHPASSTVDKLLKLEPSGPISTINCPCKECKHCPA 113
263 PNLEGGPSVFIFFPNPKIDVLMISLTPKVCVVVDVSEDDPDVQISWVFNNEVHTAQOT 322
114 SEVS---SVFIFFPKPKDVLITLTPKVCVVVDISQDDPEVHFSWFDVVEVHTAQTRP 170
323 HREDYNTIRVSTPLQIHDQDMSGKFEKCKVNNKDLPSPIERTISKIGLVRAPQVYL 382
171 PEEQFNSTFRSVSELPILHQDNLWNGRTFRCKVTSAAFPSPIEKTSRPEGTVQVHYTM 230
383 PPPAQQLSRKDVSLTCLVGFNPGDISVEVTSNGHTEENYKDTAPVLDSDSGSYFYISKLN 442
231 SPTKEEMTQSVISITCMVKGFPYDITVEMQNGQPQENYKNTPTMTDGSFYLYSKLN 290
443 MKTSKWEKTDSEFCNVRHGLKNYLYKKTISRSFGK 478
291 VKKEWQGGNFTVCSVLHEGLHHHTKSLSHSPGK 326

RESULT 13
CA_RAT
D GCA_RAT STANDARD; PRT; 322 AA.
C P20760;
T 01-FEB-1991 (Rel. 17, Created)
T 01-FEB-1991 (Rel. 17, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
T Ig gamma-2A chain C region.
S Rattus norvegicus (Rat).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
X NCBI_TaxID=10116;
N [1]
P SEQUENCE FROM N.A.
P MEDLINE=89232738; PubMed=3149946;
A Brueggemann M.;
T "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
L Gene 74:473-482(1988).
C -----
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; M33804; AAA41376.1; ALT_INIT.
R FTR; PS0019; P50019.
R HSP; P01842; 7FAB.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003597; Ig_C1.
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DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 136 196
FT DISULFID 242 300
FT CARBOHYD 172 172
SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;
N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match 43.1%; Score 1100; DB 1; Length 322;
Best Local Similarity 60.4%; Pred. No. 6.2e-71;
Matches 203; Conservative 53; Mismatches 66; Indels 14; Gaps 2;

143 AKTTPPSVYPLAPCGDITGSSVTLGCLVKGYFPEPVTVVWNSGSLSSVHTFPAVLQSG 202
1 AETTAPSYIPLAPGTALKSNMVTGLGCLVKGYFPEPVTVVWNSGSLSSVHTFPAVLQSG 60
203 LYTMSSSVTPSSWPSQTVTCVAHPASSTVDKLLKLEPSGPISTINCPCKECKHCPA 262
61 LYTLTSSVTPSSWPSQTVTCVAHPASSTVDKLLKLEPSGPISTINCPCKECKHCPA 107
263 PNLEGGPSVFIFFPNPKIDVLMISLTPKVCVVVDVSEDDPDVQISWVFNNEVHTAQOT 322
108 TGSEVS-SVFIFFPKPKDVLITLTPKVCVVVDISQDDPEVHFSWFDVVEVHTAQTHA 166
323 HREDYNTIRVSTPLQIHDQDMSGKFEKCKVNNKDLPSPIERTISKIGLVRAPQVYL 382
167 PEKQSNSTLRSVSELPVHRDLWNGRTFRCKVTSAAFPSPIEKTSRPEGTVQVHYTM 226
383 PPPAQQLSRKDVSLTCLVGFNPGDISVEVTSNGHTEENYKDTAPVLDSDSGSYFYISKLN 442
227 APPKEEMTQSVISITCMVKGFPYDITVEMQNGQPQENYKNTPTMTDGSFYLYSKLN 286
443 MKTSKWEKTDSEFCNVRHGLKNYLYKKTISRSFGK 478
287 VKKEWQGGNFTVCSVLHEGLHHHTKSLSHSPGK 322

RESULT 14
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RN Nucleic Acids Res. 10:4071-4079(1982).
[2]
RN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
[3]
RN SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
OM protein - protein search, using sw model
Run on: June 18, 2003, 16:41:57 ; Search time 34.9101 Seconds
(without alignments)
1316.302 Million cell updates/sec
Title: US-09-770-916-2
Perfect score: 2552
Sequence: 1 MAVLGLLFLVTFPSCVLSQ.....RHEGLKNYKTKTISRSPGK 478
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2067	81.0	474	1 G2MS11	Ig gamma-2b chain
2	2024.5	79.3	475	2 S01321	Ig gamma-2b chain
3	1797	70.4	405	1 G2MSBM	Ig gamma-2b chain
4	1739	68.1	446	2 S40295	Ig gamma-2a chain
5	1727.5	67.7	469	2 S37483	Ig gamma-2a chain
6	1485.5	58.2	444	2 PC4436	monoclonal antibody
7	1456.5	57.1	472	2 S31459	Ig gamma-1 chain
8	1427.5	55.9	470	2 S22080	Ig heavy chain pre
9	1419	55.6	330	1 G2MSA	Ig gamma-2a chain
10	1414	55.4	399	1 G2MSGM	Ig gamma-2a chain
11	1385.5	54.3	335	1 G2MSAB	Ig gamma-2a chain
12	1326.5	52.0	333	2 PS0018	Ig gamma-2b chain
13	1202.5	47.1	329	2 S00847	Ig gamma-2c chain
14	1170	45.8	329	1 G3MSC	Ig gamma-3 chain C
15	1159	45.4	398	1 G3MSW	Ig gamma-3 chain C
16	1150	45.1	324	1 G1MS	Ig gamma-1 chain C
17	1145	44.9	393	1 G1MSM	Ig gamma-1 chain C
18	1112	43.6	326	2 PS0017	Ig gamma-1 chain C
19	1100	43.1	322	2 PS0019	Ig gamma-1 chain C
20	1087	42.6	330	1 GHRU	Ig gamma-2a chain
21	1080.5	42.3	323	1 GHRB	Ig gamma-1 chain C
22	1080.5	42.3	329	1 G2GP	Ig gamma chain C r
23	1072.5	42.0	377	2 A60764	Ig gamma-3 chain C
24	1072.5	42.0	377	2 A23511	Ig gamma-3 chain C
25	1059	41.5	326	1 G2HU	Ig gamma-2 chain C
26	1058	41.5	328	2 I47159	Ig gamma 2a chain C
27	1054.5	41.3	327	1 G4HU	Ig gamma-4 chain C
28	1053	41.3	374	2 S69339	Ig heavy chain V r
29	1049	41.1	328	2 I47160	Ig gamma 2b chain

30	1039	40.7	548	2 S38864	Ig epsilon chain C
31	1036	40.6	231	2 PC4155	Ig gamma-2b chain
32	1028	40.3	328	2 I47161	Ig gamma 3 chain c
33	1023.5	40.1	308	2 C30554	Ig heavy chain C r
34	1022	40.0	327	2 I47158	Ig gamma 1 chain c
35	987.5	38.7	327	2 S06611	Ig gamma-2 chain C
36	921	36.1	246	2 S38950	Ig gamma chain - m
37	884	34.6	277	2 I47162	Ig gamma 4 chain c
38	840.5	32.9	549	2 S04845	Ig heavy chain pre
39	831	32.6	213	2 S68213	Ig heavy chain (Ma
40	781.5	30.6	255	4 S31866	Ig gamma-1 chain C
41	774.5	30.3	234	2 PT0207	Ig gamma chain C r
42	774	30.3	627	2 S14683	Ig gamma chain C r
43	772.5	30.3	289	1 G3HUI	Ig mu chain precur
44	772.5	30.3	592	2 S25705	Ig mu chain - shee
45	751	29.4	572	2 B46529	Ig Y heavy chain (

ALIGNMENTS

RESULT 1
G2MS11

Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific
A:Reference number: S25057
A:Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A>Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A>Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and 9
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Accession: A26233
A:Contents: b allele
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL
A:Cross-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah
J. Biol. Chem. 269, 12345-12350, 1994

Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 Reference number: A53598; MUID:94216359; PMID:7512967
 Accession: A53598
 Status: preliminary
 Molecule type: protein
 Residues: 234-251 <KIM>
 Comment: The a allele sequence is shown.

Genetics:
 Introns: 138/1; 236/1; 258/1; 368/1
 Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) in disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la Superfamily: immunoglobulin C region; immunoglobulin homology
 Keywords: 'alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin 157-222/Domain: immunoglobulin homology <IM1>
 236-257/Region: hinge
 281-350/Domain: immunoglobulin homology <IM2>
 387-454/Domain: immunoglobulin homology <IM3>
 152/Disulfide bonds: interchain (to light chain) #status predicted
 164-220,288-348,394-452/Disulfide bonds: #status predicted
 247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 324/Binding site: carbohydrate (asn) #status predicted

Query Match 81.0%; Score 2067; DB 1; Length 474;
 Best Local Similarity 83.8%; Pred. No. 1.1e-117;
 Matches 389; Conservative 29; Mismatches 38; Indels 8; Gaps 4;

17 VLSQVQLKQSGPGLVQPQSLITCTVSGFSLTSYGVHWRQSPGKGLWLVGIVWSGD- 75
 17 VHSEYQLQSGPELVNPGASVMSKASGYITFTYHWRVQKPGQGLEWIGYINPNKDG 76
 76 TDYNAAFISRLSISKDNKSKQLFFKMNLSLRATDTAIYVCARNRGDIYYDYFYAMDYWGQ 135
 77 TKFNKFKGKATLTSDKSNATAYMELSSLTSEDSAVYFCARD-----DYDW-FAYWGQ 130
 136 TSVTVSSAKTTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF 195
 131 TLTVTSAKATTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTL 190
 196 -PALLOSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDVKLEPSPGISTINPCPC 254
 191 SQALLQSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDVKLEPSPGISTINPCPC 250
 255 KECHKCAPNLGGPSVFIFPPNPKDVLMSLTLPKVTCTVVDVSDDDPDVQISWVFNVE 314
 251 KECHKCAPNLGGPSVFIFPPNPKDVLMSLTLPKVTCTVVDVSDDDPDVQISWVFNVE 310
 315 VHTAQQTQTHREDYNSIRVYVSTLPIQHDMWSGKFKCKVNNKDLPSPIERTISKIGLV 374
 311 VHTAQQTQTHREDYNSIRVYVSTLPIQHDMWSGKFKCKVNNKDLPSPIERTISKIGLV 370
 375 RAPQVYILPPPAQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS 434
 371 RAPQVYILPPPAQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS 430
 435 YFIYSKLNMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 478
 431 YFIYSKLNMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 474

RESULT 2
 Ig gamma-2b chain precursor - mouse
 Species: Mus musculus (house mouse)
 Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 Accession: S01321
 Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 ir. J. Biochem. 176, 287-295, 1988
 Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
 Reference number: S01320; MUID:88329081; PMID:3138116
 Accession: S01321
 Molecule type: mRNA
 Residues: 1-475 <DE1>
 Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781

A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMV>

Query Match 79.3%; Score 2024.5; DB 2; Length 475;
 Best Local Similarity 82.3%; Pred. No. 4.2e-115;
 Matches 381; Conservative 30; Mismatches 47; Indels 5; Gaps 2;

17 VLSQVQLKQSGPGLVQPQSLITCTVSGFSLTSYGVHWRQSPGKGLWLVGIVWSG-GD 75
 17 VOSQVQLQSGAELARPCASVLSKASGYITFTYHWRVQKPGQGLEWIGIYPPGSSN 76
 76 TDYNAAFISRLSISKDNKSKQLFFKMNLSLRATDTAIYVCARNRGDIYYDYFYAMDYWGQ 135
 77 SYFNEKFKGKATLTVDKSSSTAYLHLSLTSEDSAVYFCAGPRQVGLLPF----GYWGQ 132
 136 TSVTVSSAKTTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF 195
 133 TLVTASAAKATTPPSVYPLAPGCGDPTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTF 192
 196 PALLOSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDVKLEPSPGISTINPCPC 255
 193 PALLOSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVDVKLEPSPGISTINPCPC 252
 256 ECHKCAPNLGGPSVFIFPPNPKDVLMSLTLPKVTCTVVDVSDDDPDVQISWVFNVE 315
 253 ECHKCAPNLGGPSVFIFPPNPKDVLMSLTLPKVTCTVVDVSDDDPDVQISWVFNVE 312
 316 HTAQQTQTHREDYNSIRVYVSTLPIQHDMWSGKFKCKVNNKDLPSPIERTISKIGLV 375
 313 LTAQQTQTHREDYNSIRVYVSTLPIQHDMWSGKFKCKVNNKDLPSPIERTISKIGLV 372
 376 APQVYILPPPAQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS 435
 373 APQVYILPPPAQLSRKDVSLTCLVGFNPGDISVEMTSNGHTENYKDTAPVLDSDGS 432
 436 FIYSKLNMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 478
 433 FIYSKLNMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 475

RESULT 3
 G2B5M
 Ig gamma-2b chain C region, membrane-bound form - mouse
 Species: Mus musculus (house mouse)
 Date: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
 Accession: C02154; A02158; B02157
 R.Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
 Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
 Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglob
 A:Reference number: A02154; MUID:82222190; PMID:6283537
 Accession: C02154
 Molecule type: DNA
 A:Residues: 335-405 <YAM>
 A:Cross-references: GB:J00462
 R.Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wa
 Cell 26, 19-27, 1981
 Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma
 A:Reference number: A02158; MUID:82115295; PMID:6799207
 Accession: A02158
 A:Molecule type: DNA
 A:Residues: 335-378 <ROG>
 A:Note: the translation of the first exon of the membrane-bound segment is given
 R.Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 Accession: B02157
 A:Contents: a allele.
 A:Molecule type: DNA

A:Residues: 1-335, 'K' <YA2>
 C:Comment: The sequence of residues 1-334 was assumed to be identical with the corresponding C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The major one has an alternative 3' end, encoded in separate exons, that is homologous with the sequence of residues 1-334.
 C:Genetics:
 A:Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin
 F:143-212/Domain: immunoglobulin homology <IM>
 F:352-369/Domain: transmembrane #status predicted <TM>
 F:370-405/Domain: intracellular #status predicted <INT>
 F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.4%; Score 1797; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.9e-101;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 AKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPALQSG 202
 Db 1 AKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPALQSG 60

QY 203 LYTMSSSVTPSSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECHKCPA 262
 Db 61 LYTMSSSVTPSSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECHKCPA 120

QY 263 PNLEGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDVQISWVNNVEVHTAQTOT 322
 Db 121 PNLEGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDVQISWVNNVEVHTAQTOT 180

QY 323 HREDYNSIRVYVSTLPIQHDWMSGKEFKCKYNNKDLPSPIERTISKIKGLVRAPQVYIL 382
 Db 181 HREDYNSIRVYVSTLPIQHDWMSGKEFKCKYNNKDLPSPIERTISKIKGLVRAPQVYIL 240

QY 383 PPPAQSLRKDVSLTCLVGVNPGDISEWTSNGHTEENYKDTAPVLDSDGSYFYISKLN 442
 Db 241 PPPAQSLRKDVSLTCLVGVNPGDISEWTSNGHTEENYKDTAPVLDSDGSYFYISKLN 300

QY 443 MKTSKWEKTSFSCNVRHEGLKNYLLKRTISRSPG 477
 Db 301 MKTSKWEKTSFSCNVRHEGLKNYLLKRTISRSPG 335

RESULT 4
 S40295
 Ig gamma-2a chain (mAb735) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
 C:Accession: S40295
 Submitted to the EMBL Data Library, January 1993
 A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
 A:Reference number: S40295
 A:Accession: S40295
 A:Molecule type: protein
 A:Residues: 1-446 <KLE>
 A:Genetics:
 A:Map position: 12
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglytamic acid
 F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
 F:1-117/Domain: V-D-J region <VDJ>
 F:118-446/Domain: C region <CH>
 F:118-214/Domain: C1 region <CH1>
 F:215-230/Region: hinge
 F:231-340/Domain: C2 region <CH2>
 F:341-446/Domain: C3 region <CH3>
 F:360-427/Domain: immunoglobulin homology <IM>
 F:428-446/Domain: immunoglobulin homology <IM>
 F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
 F:132/Disulfide bonds: interchain (to light chain) #status predicted
 F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 68.1%; Score 1739; DB 2; Length 446;
 Best Local Similarity 70.4%; Pred. No. 6.8e-98;
 Matches 323; Conservative 56; Mismatches 66; Indels 14; Gaps 4;

QY 20 QVQLKQSGPGLVQPSQSLSTCTVSGFSLTSYGVHVVRQSPGKGLWLVWSG-GPTDY 78
 Db 1 QIQLQSGPGLVQPSQSLSTCTVSGFSLTSYGVHVVRQSPGKGLWLVWSG-GPTDY 60

QY 79 NAAFIISRLSISKDNSKLSQFLFKMNSLRATDTAIYICARNRGDIYDYFTYAMDYWGQTSV 138
 Db 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAYVFCARGG-----KPFAMDYWGQTSV 113

QY 139 TVSSAKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPAL 198
 Db 114 TVSSAKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPAL 173

QY 199 LOSGLTMSSTVTPSSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECH 258
 Db 174 LOSGLTMSSTVTPSSTWPSQVTCVAHPASSTVVDKLEPSGPISTINPCPPCKECH 227

QY 259 KCPAPNLEGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDVQISWVNNVEVHTA 318
 Db 228 KCPAPNLEGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDVQISWVNNVEVHTA 287

QY 319 QTQTHREDYNSIRVYVSTLPIQHDWMSGKEFKCKYNNKDLPSPIERTISKIKGLVRAP 378
 Db 288 QTQTHREDYNSIRVYVSTLPIQHDWMSGKEFKCKYNNKDLPSPIERTISKIKGLVRAP 347

QY 379 VYLPPPAQLSRKDVSLTCLVGVNPGDISEWTSNGHTEENYKDTAPVLDSDGSYFYI 438
 Db 348 VYLPPPAQLSRKDVSLTCLVGVNPGDISEWTSNGHTEENYKDTAPVLDSDGSYFYI 407

QY 439 SKLNKTSKWEKTSFSCNVRHEGLKNYLLKRTISRSPG 477
 Db 408 SKLRVEKKNNVVERNSYSCSVVHGLEHNNHTTSFSRTPG 446

RESULT 5
 S37483
 Ig gamma-2a chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37483
 R:Decancel, F.F.D.
 Submitted to the EMBL Data Library, February 1993
 A:Reference number: S37483
 A:Accession: S37483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-469 <DUC>
 C:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:276-345/Domain: immunoglobulin homology <IM>

Query Match 67.7%; Score 1727.5; DB 2; Length 469;
 Best Local Similarity 69.6%; Pred. No. 3.6e-97;
 Matches 320; Conservative 60; Mismatches 69; Indels 11; Gaps 4;

QY 20 QVQLKQSGPGLVQPSQSLSTCTVSGFSLTSYGVHVVRQSPGKGLWLVWSG-GPTDY 78
 Db 20 QIQLQSGPGLVQPSQSLSTCTVSGFSLTSYGVHVVRQSPGKGLWLVWSG-GPTDY 79

QY 79 NAAFIISRLSISKDNSKLSQFLFKMNSLRATDTAIYICARNRGDIYDYFTYAMDYWGQTSV 138
 Db 80 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAYVFCARGGAT----AFLLDYWGQTSV 135

QY 139 TVSSAKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPAL 198
 Db 136 TVSSAKTTPSVYPLAPGCGDTTSSVTGLCLVKGYPFVSPTVWNSGLSSSVHFPAL 195

C;Accession: PS0018; B25941
R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MUID:89232738; PMID:3149946
A;Accession: PS0018
A;Molecule type: DNA
A;Residues: 1-333 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079; 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: B25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 227-333 <BR2>
C;Genetics:
A;Introns: 96/1; 117/1; 227/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F:20-82/Domain: immunoglobulin homology <IMM>

Query Match 52.0%; Score 1326.5; DB 2; Length 333;
Best Local Similarity 73.6%; Pred. No. 4e-73;
Matches 248; Conservative 34; Mismatches 50; Indels 5; Gaps 3;

QY 143 AKTTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 202
Db 1 ARTTAPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 60
QY 203 LYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLE-PSGPISTINPCPKCKCHKCP 261
Db 61 LYTLSSVT--SSTWPSQVTCVAHPASSTVDKLE-PSGPISTINPCPKCKCHKCP 116
QY 262 APNLEGGPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 321
Db 117 VPELLGGPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 176
QY 322 THREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 381
Db 177 PREEQYNSTIRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 236
QY 382 LPPPAEQLSKDVSLTCLVGVNPGDISVETNSGHTENYKDTAPVLDSDGSYFIYSKL 441
Db 237 MGPTTEQTEQVSLTCLVGVNPGDISVETNSGHTENYKDTAPVLDSDGSYFIYSKL 296
QY 442 NMKTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478
Db 297 NVERSRWDSRAPFVCSVYHGLNHHHVEKISRPPGK 333

RESULT 13
S00847
Ig gamma-2c chain C region - rat (fragment)
Species: Rattus norvegicus (Norway rat)
Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
Accession: S00847
Eur. J. Immunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext
A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847
A;Molecule type: mRNA
A;Residues: 1-329 <BRU>
C;Cross-references: EMBL:X07189; NID:57602; PID:CAA30169.1; PID:g663228
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F:20-84/Domain: immunoglobulin homology <IMM>

Query Match 47.1%; Score 1202.5; DB 2; Length 329;
Best Local Similarity 68.2%; Pred. No. 1.2e-65;
Matches 229; Conservative 35; Mismatches 65; Indels 7; Gaps 4;

QY 143 AKTTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 202
Db 1 ARTTAPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 60
QY 203 LYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKLE-PSGPISTINPCPKCKCHKCPA 262
Db 61 LYTLSSVTVPSSSTWPSQVTCVAHPASSTVDKLE-PSGPISTINPCPKCKCHKCPA 114
QY 263 PNLEGGPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 322
Db 115 DNL-GRPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 173
QY 323 HREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 382
Db 174 HEQLNGTFRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 233
QY 383 PPAEQLSKDVSLTCLVGVNPGDISVETNSGHTENYKDTAPVLDSDGSYFIYSKL 442
Db 234 PPREQMSKNKVSILTCVTSFYPSISVEWNGELQDQKNTLPVLDSDGSYFIYSKL 293
QY 443 MKTSKWEKTDSCFNVRHEGLKNYLLKKTISRSPGK 478
Db 294 VPTDSWNRGDIYTCVSVHGLNHHHVEKISRPPGK 329

RESULT 14
G3M5C
Ig gamma-3 chain C region, secreted form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: B02156
R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Bl
EMBO J. 3, 2041-2046, 1984
A;Title: Structure analysis of the murine IgG3 constant region gene.
A;Reference number: A02156; MUID:85027161; PMID:6092053
A;Accession: B02156
A;Molecule type: DNA
A;Residues: 1-329 <WEL>
A;Cross-references: GB:J00451
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Introns: 97/1; 113/1; 223/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
F:19-83/Domain: immunoglobulin homology <IMI>
F:97-112/Region: hinge
F:136-205/Domain: immunoglobulin homology <IM2>
F:242-309/Domain: immunoglobulin homology <IM3>
F:179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.8%; Score 1170; DB 1; Length 329;
Best Local Similarity 66.2%; Pred. No. 1.1e-63;
Matches 221; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

QY 145 TTPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 204
Db 2 TTAPSVYPLAPGCGDTTSSVTLGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 61
QY 205 TMSSSVTPSPSTWPSQVTCVAHPASSTVDKLE-PSGPISTINPCPKCKCHKCP 264
Db 62 SLSSLVTPSPSTWPSQVTCVNAHPASSTVDKLE-PSGPISTINPCPKCKCHKCP 115
QY 265 LEGGPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 324
Db 116 ILGGPSVFIFPPNIDKLVMSLTGCLVKGYPESVTVTWNSGLSSSVHFFPALLQSG 175
QY 325 EDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 384
Db 176 AQYNSTIRVSTLPIQHODWMSGKEFKCKVNNKALPSPTEIKTSKPKGLVRAPQVY 235
QY 385 PPAEQLSKDVSLTCLVGVNPGDISVETNSGHTENYKDTAPVLDSDGSYFIYSKL 444

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 56.3933 Seconds
(without alignments)
2164.388 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVLGLFCLVFPSCVLSQ.....RHEGLKNYKLTISRSPGK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1156168 seqs, 255349102 residues

Total number of hits satisfying chosen parameters: 1156168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1666.5	65.3	469	6	US-10-429-662-10
2	1666.5	65.3	469	6	US-10-429-660-10
3	1643	64.4	468	1	PCT-US02-02373-12
4	1565.5	61.3	446	5	US-09-618-380A-7
5	1497.5	58.7	462	1	PCT-US02-34420A-23
6	1497.5	58.7	462	1	PCT-US02-35333A-23
7	1497.5	58.7	462	6	US-10-286-132A-23
8	1497.5	58.7	462	6	US-10-281-479A-23
9	1472	57.7	464	6	US-10-275-180A-23
10	1472	57.7	464	6	US-10-384-933-9
11	1462.5	57.3	361	6	US-10-272-899A-82
12	1457	57.1	474	1	PCT-US02-36107-14
13	1457	57.1	474	6	US-10-292-088-14
14	1452.5	56.9	361	6	US-10-272-899A-80
15	1451	56.9	466	1	PCT-US02-36107-70
16	1451	56.9	466	6	US-10-292-088-70
17	1449	56.8	466	1	PCT-US02-36107-22
18	1449	56.8	466	6	US-10-292-088-22
19	1449	56.8	466	1	PCT-US02-36107-86
20	1449	56.8	466	6	US-10-292-088-86
21	1448	56.7	466	1	PCT-US02-36107-30
22	1448	56.7	466	6	US-10-292-088-30
23	1446	56.7	451	1	PCT-US03-13054-4
24	1446	56.7	451	6	US-10-423-299-4
25	1445.5	56.6	469	1	PCT-US03-10154-72
26	1445.5	56.6	469	6	US-10-404-724-72

ALIGNMENTS

RESULT 1

US-10-429-662-10

; Sequence 10, Application US/10429662

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Compositions For Nucleic Acid Delivery

; FILE REFERENCE: 2537.000010

; CURRENT APPLICATION NUMBER: US/10/429,662

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 469

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-662-10

Query Match 65.3%; Score 1666.5; DB 6; Length 469;

Best Local Similarity 66.2%; Pred. No. 1e-99;

Matches 317; Conservative 62; Mismatches 89; Indels 11; Gaps 5;

QY	1	MAVLGLFCLVFPSCVLSQVQLKQSGPGLVPSQSLTCTVSGFSLTSGVGHVWRQSP	60
DB	1	MAVLGLFCLVFPSCVLSQVHLKESGPGVAPQSLSITCTVSGFSLTSGVGHVWRQPP	60
QY	61	KGKLEWLGVIWGGDTDYNAAFISRLSISKDNKSQLEFFKMNLSRATDAIYYCARNRGD	120
DB	61	KGKLEWLGVIWGGDTDYNSALMSRLSINKDNKSQVFLKMNLSLQADDAIYYCARFRA	120
QY	121	IYDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTTGSSTVPLGCLVKGYFPESVT	180
DB	121	SYVD--YAVDYWGQGTSTVTVSS--TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPT	177
QY	181	VTVNWSGLSSSVHTFPALIQ-SGLYTMSSSVTVPSSTWPSQVITCVSAHPASSTVDKKL	239
DB	178	VSNWSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSTWPSQVITCVSAHPASSTVDKKL	237
QY	240	EPSGPISITINPCPCKECHKCAPNLEGPSVFIFPPNKKIVMLISLTPKVCVVVDVSE	299
DB	238	EPKSCDKT-HTCPP-----CPAPELLGPGSPVLEFPKPKDPTLMISRTPEVTCVVVDVSH	290
QY	300	DDPDQVQISWFMNVVHTAOTQOTREDYNSTIRVYSTLPPIQHDWMSGKEFKCKVNNKDL	359
DB	291	EDPEVKFWYVDGVEVHNAKTPREEQYNSTIRVYSTLPPIQHDWMSGKEFKCKVNNKAL	350
QY	360	PSPIERTISKIKGLVRAQVYILPPPAEQLSKDVSCLVYVGENPGDTSVETWNGHTE	419
DB	351	PAPIEKTISKAKGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPE	410

Query Match 61.3%; Score 1565.5; DB 5; Length 446;
Best Local Similarity 64.1%; Pred. No. 3.2e-93;
Matches 295; Conservative 63; Mismatches 87; Indels 15; Gaps 4;
QY 20 QVQLKSGPGLVQPSQSLSTCTVSGFSLTSYGVHVRQSPGKGLWLGVIWGGDDTNYN 79
Db 1 QVQLKSGPGLVQPSQSLSTCTVSGFSLTSYGVHVRQSPGKGLWLGVIWGGDDTNYN 60
QY 80 AAFISRLTSKDKNSKQSLFFKMSLRATDIAIYCCARNRGGDIYDFTYAMDYWGQGTSTV 139
Db 61 AAFISRLTSKDKNSKQSLFFKMSLRATDIAIYCCARNRGGDIYDFTYAMDYWGQGTSTV 113
QY 140 VSSAKTPPSVPLAPGCGDTTSSVTGLGKLVKGYPPESVTVWNSGSLSSSVHTTPALL 199
Db 114 VSSAKTPPSVPLAPGCGDTTSSVTGLGKLVKGYPPESVTVWNSGSLSSSVHTTPALL 199
QY 200 Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTVDDKKLEPSGPISTINPCPKCECH 258
Db 174 Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTVDDKKLEPSGPISTINPCPKCECH 227
QY 259 KCPAPNLEGGPSVFIPPPNIKDVIMSLTPKVTCTVVDVSDPDVQISWFFVNNVHTA 318
Db 228 -CPAPNLEGGPSVFIPPPNIKDVIMSLTPKVTCTVVDVSDPDVQISWFFVNNVHTA 286
QY 319 QVTHREDYNSIRVSTLPIQHDHMSKCKKYNKDLPSPIERTISKIKGLVRAPQ 378
Db 287 KTKPREQYNSIRVSTLPIQHDHMSKCKKYNKDLPSPIERTISKIKGLVRAPQ 346
QY 379 VYLPPAPOLSKDKVSLTCLVGVGPNQDISVETWNSGHTENYKDTAPVLDSDGSYFYI 438
Db 347 VYLPPAPOLSKDKVSLTCLVGVGPNQDISVETWNSGHTENYKDTAPVLDSDGSYFYI 406
QY 439 SKLNKMTSKWEKTDSCFNVRHEGLKNYLLKTKTISRSPGK 478
Db 407 SKLTVDKSRWQOGNVSFSCVMHEALHNHYTKQSLSLSPGK 446

RESULT 5
PCT-US02-34420A-23
; Sequence 23, Application PC/TUS0234420A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACTOR-
; FILE REFERENCE: 21085.0029P3
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US02/34420A
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
PCT-US02-34420A-23

Query Match 58.7%; Score 1497.5; DB 1; Length 462;
Best Local Similarity 61.1%; Pred. No. 8.1e-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;

Best Local Similarity 61.1%; Pred. No. 8.1e-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;
QY 4 LGLLFCVLTTPSCVLSQVQLKQSGPGLVQPSQSLSTCTVSGFSLTSYGVHVRQSPGK 63
Db 5 LSLFL-LVLVLKQVCEVLMVSGGLVLPKGGSLKLSAASGFTFSYVMSVWRQTPEKR 63
QY 64 LEWLGVTWGGD-TDYNAAFISRLTSKDKNSKQSLFFKMSLRATDIAIYCCARNRGGDIY 122
Db 64 LEWVATISSGSGSYTYPDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYICAR-RG--- 119
QY 123 YDTYAMDYWGQGTSTVTVSSAKTTPPSVPLAPGCGDTTSSVTGLGKLVKGYPPESVTV 182
Db 120 -DSMITTDYWGQGTSTVTVSSAKTTPPSVPLAPGCGDTTSSVTGLGKLVKGYPPESVTV 178
QY 183 WNSGSLSSSVHTTPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTVDDKKLEPS 242
Db 179 WNSGSLSSSVHTTPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTVDDKKLEPS 237
QY 243 GPISTINPCPKCECHKCAPNLEGGPSVFIPPPNIKDVIMSLTPKVTCTVVDVSDPD 302
Db 238 -----RDC-GCKPC-ICTVPEVS--SVFIFPPKPKDVLITITLTPKVTCTVVDVSDPD 286
QY 303 DVQISWFFVNNVHTAQTQTHREDYNSIRVSTLPIQHDHMSKCKKYNKDLPSPIERTISKIKGLVRAPQ 362
Db 287 EVQSFVDEVDVHTAQTQTHREDYNSIRVSTLPIQHDHMSKCKKYNKDLPSPIERTISKIKGLVRAPQ 346
QY 363 IERTISKIKGLVRAPQVYIILPPAEQLSRKDVSLTCLVGVGPNQDISVETWNSGHTENY 422
Db 347 IERTISKIKGLVRAPQVYIILPPAEQLSRKDVSLTCLVGVGPNQDISVETWNSGHTENY 406
QY 423 KDTAPVLDSDGSYFYIYKLNKMTSKWEKTDSCFNVRHEGLKNYLLKTKTISRSPGK 478
Db 407 KNTQPIMDTDGSGYFYIYKLNKMTSKWEKTDSCFNVRHEGLKNYLLKTKTISRSPGK 462

RESULT 6
PCT-US02-35333A-23
; Sequence 23, Application PC/TUS0235333A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; FILE REFERENCE: 21085.0029P2
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US02/35333A
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
PCT-US02-35333A-23

Query Match 58.7%; Score 1497.5; DB 1; Length 462;
Best Local Similarity 61.1%; Pred. No. 8.1e-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;

5 LSLIF-LVLVLKGVQCEVLMVESGGLVKGPGSLKLSCAASGFTFSYVMSWVRQTPK 63
64 LEWLGVIWSGGD-TDYNAAFISRLSISKDNKSQSLFKMNSLRATDTAIYYCARNRDIY 122
64 LEWVATISSGGSYTYYPDSVAGKRTISRDNKNTLYLQMSLSRSEDITAMYCAR-RG--- 119
123 YDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTGSSVTLGCLVKGYEPESVTVT 182
120 -DSMTITDYGQGTTLTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYEPPEVTVT 178
183 WNSGSLSSSVHTEFALLQSLYTNSSSVTVPSSTWPSOTVTCVAHPASSTTVDKKLEPS 242
179 WNSGSLSSGVHTFAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTTVDKKIYP- 237
243 GPISTINPCPKCKECHKCAPNLEGGPSVFPPPNKIDVLMISLTPKVTVCVVVDVSEDDP 302
238 -----RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLITLTPKVTVCVVVDISKDDP 286
183 WNSGSLSSSVHTEFALLQSLYTNSSSVTVPSSTWPSOTVTCVAHPASSTTVDKKLEPS 242
179 WNSGSLSSGVHTFAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTTVDKKIYP- 237
243 GPISTINPCPKCKECHKCAPNLEGGPSVFPPPNKIDVLMISLTPKVTVCVVVDVSEDDP 302
238 -----RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLITLTPKVTVCVVVDISKDDP 286
303 DVQISWFNNVEVHTAQTQTHREDYNSTIRVSTLPIQHDQMSKCKEFCVNNKDLSP 362
287 EVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVELPIMHODWLNKKEFCRVNSAFAFAP 346
363 IERTISKIGLVRAPQVYILPPAPQSLRKVDVSLTCLVVGPNPGLDISVETWSNGHTEENY 422
347 IERTISKIGLVRAPQVYILPPAPQSLRKVDVSLTCLVVGPNPGLDISVETWSNGHTEENY 406
423 KDTAPVLDSDGSFYFYISKLNKMTSKWEKTDSPSCNVRHEGLKNLYLKKTIISRSPGK 478
407 KNTQPIMDTDSGYFYISKLNKMTSKWEKTDSPSCNVRHEGLKNLYLKKTIISRSPGK 462

RESULT 7
3-10-286-132A-23
Sequence 23, Application US/10286132A
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimbely, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002907
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
S-10-286-132A-23

Query Match 58.7%; Score 1497.5; DB 6; Length 462;
Best Local Similarity 61.1%; Pred. No. 8.le-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;
4 LGLFCLVTFPPSCVLQVQLKQSGPGLVQPSQSLITCTVSGFSLTSGYVHWVRQSPGK 63
5 LSLIF-LVLVLKGVQCEVLMVESGGLVKGPGSLKLSCAASGFTFSYVMSWVRQTPK 63
64 LEWLGVIWSGGD-TDYNAAFISRLSISKDNKSQSLFKMNSLRATDTAIYYCARNRDIY 122
64 LEWVATISSGGSYTYYPDSVAGKRTISRDNKNTLYLQMSLSRSEDITAMYCAR-RG--- 119

123 YDFTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPGCGDTGSSVTLGCLVKGYEPESVTVT 182
120 -DSMTITDYGQGTTLTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYEPPEVTVT 178
183 WNSGSLSSSVHTEFALLQSLYTNSSSVTVPSSTWPSOTVTCVAHPASSTTVDKKLEPS 242
179 WNSGSLSSGVHTFAVLQSDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTTVDKKIYP- 237
243 GPISTINPCPKCKECHKCAPNLEGGPSVFPPPNKIDVLMISLTPKVTVCVVVDVSEDDP 302
238 -----RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLITLTPKVTVCVVVDISKDDP 286
303 DVQISWFNNVEVHTAQTQTHREDYNSTIRVSTLPIQHDQMSKCKEFCVNNKDLSP 362
287 EVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVELPIMHODWLNKKEFCRVNSAFAFAP 346
363 IERTISKIGLVRAPQVYILPPAPQSLRKVDVSLTCLVVGPNPGLDISVETWSNGHTEENY 422
347 IERTISKIGLVRAPQVYILPPAPQSLRKVDVSLTCLVVGPNPGLDISVETWSNGHTEENY 406
423 KDTAPVLDSDGSFYFYISKLNKMTSKWEKTDSPSCNVRHEGLKNLYLKKTIISRSPGK 478
407 KNTQPIMDTDSGYFYISKLNKMTSKWEKTDSPSCNVRHEGLKNLYLKKTIISRSPGK 462

RESULT 8
US-10-281-479A-23
Sequence 23, Application US/10281479A
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimbely, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
US-10-281-479A-23

Query Match 58.7%; Score 1497.5; DB 6; Length 462;
Best Local Similarity 61.1%; Pred. No. 8.le-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;
4 LGLFCLVTFPPSCVLQVQLKQSGPGLVQPSQSLITCTVSGFSLTSGYVHWVRQSPGK 63
5 LSLIF-LVLVLKGVQCEVLMVESGGLVKGPGSLKLSCAASGFTFSYVMSWVRQTPK 63
64 LEWLGVIWSGGD-TDYNAAFISRLSISKDNKSQSLFKMNSLRATDTAIYYCARNRDIY 122
64 LEWVATISSGGSYTYYPDSVAGKRTISRDNKNTLYLQMSLSRSEDITAMYCAR-RG--- 119

411 TOPIMNTNGSYFVYSKLVNQKSNWEAGNTFTCSVLHGLHNHHTKSLSHSPGK 464

RESULT 11

Sequence 82, Application US/10272899A

GENERAL INFORMATION:

APPLICANT: O'Keefe, Theresa L.

APPLICANT: Healy, Judith Jacques

APPLICANT: Newman, Walter

APPLICANT: Ponath, Paul

APPLICANT: Bruce Keyt

TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,

TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF

TITLE OF INVENTION: USE THEREFOR

FILE REFERENCE: MP101-244P2RM

CURRENT APPLICATION NUMBER: US/10/272,899A

CURRENT FILING DATE: 2002-10-17

PRIOR APPLICATION NUMBER: 60/350,166

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: 60/392,364

PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82

LENGTH: 361

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: immunoglobulin cassette protein sequence

OTHER INFORMATION: Leader-Mu_WT_60

0-770-916-2

Query Match 57.3%; Score 1462.5; DB 6; Length 361;
Best Local Similarity 59.8%; Pred. No. 1.1e-86;
Matches 286; Conservative 35; Mismatches 40; Indels 117; Gaps 2;

1 MAVGLLFLCLVTPNCVLSRL----- 21

61 GKGLEWLVHSGDGDYNAAFISRLISKDNKSKQLFFKMSLRATDAIYYCARNRGD 120

22 ----- 21

121 IYYDFTYAMYWGQGTSVTVSSAKTTPPSVYPLAPCGDGTGSSVTGLGCLVKGYFPESVT 180

22 -----VTVSSAKTTPPSVYPLAPCGDGTGSSVTGLGCLVKGYFPPEVT 64

181 VTWNSGLSSSVHTEFALLQSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLE 240

65 LTWNSGLSSSVHTEFALLQSGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLE 124

241 PSGPSTINPCPPCKECHKCPAPNLEGGPSVFIPPNIKDVLMLISLTPKVTVCVVVDVSED 300

125 PRVPI-TQNPCPPLKECPCAAPDLGLGSPSVFIPPKIKDVLMLISLTPKVTVCVVVDVSED 183

301 DPDVQISWVFNVEVHTAQTQTHREDYNTIRVSTLPVHODWMSGKBEKCKVNNKDL 360

184 DPDVQISWVFNVEVHTAQTQTHREDYNTIRVSTLPVHODWMSGKBEKCKVNNKDL 243

361 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVETWSNGHTE 420

244 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVETWSNGHTE 303

421 NYKDTAPVLDSDGSYFIYKLNKMTSKWEKTSFSCNVRHEGLNHYLTKTISRSPGK 478

304 NYKNTATVLDSDGSYFIYKLNKMTSKWEKTSFSCNVRHEGLNHYLTKTISRSPGK 361

RESULT 12

Ct-US02-36107-14

Sequence 14, Application PC/TUS0236107

GENERAL INFORMATION:

APPLICANT: ABGENIX, INC.

APPLICANT: PFIZER PRODUCTS INC.

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 PCT

CURRENT APPLICATION NUMBER: PCT/US02/36107

CURRENT FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 474

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US02-36107-14

Query Match 57.1%; Score 1457; DB 1; Length 474;

Best Local Similarity 58.6%; Pred. No. 3.4e-86;

Matches 280; Conservative 72; Mismatches 104; Indels 22; Gaps 7;

QY 10 LVTFPSCVLSQVOLKQSGPLVQPSQSLTCTVSGFSLTSGVHVVRQSPGKLEWLV 69

Db 10 LVALLRGVQCQVQLVESGGVGVQPSRLSLCAASGFTFSSYGMHVVRQAPCGKLEWAV 69

QY 70 IWSGGDTDYNAAFI-SRLISKDNKSKQLFFKMSLRATDAIYYCAR-----NRGDI 121

Db 70 ISNDGDNKYHADSVNGRFTISRDNRSRTLYLQMSLRADTAIVYCCARRGMGSSGSRGDY 129

QY 122 YDFTYAMYWGQGTSVTVSSAKTTPPSVYPLAPCGDGTGSSVTGLGCLVKGYFPESVT 181

Db 130 YY--YYGLDWGQGTTVTVSSASTKGPSVFELAPCSRSTSESTAALGCLVKGYFPPEVT 187

QY 182 TWNSGLSSSVHTEFALLQ-SGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVVDKLE 240

Db 188 SWSGALTSGVHTFPAVLSQSLYSLSSVTVPSSTWPSQTVTCVAHPASSTVVDKLE 247

QY 241 PSGPSTINPCPPCKECHKCPAPNLEGGPSVFIPPNIKDVLMLISLTPKVTVCVVVDVSED 300

Db 248 -----RKC--CVCPCPPAPPV-AGPSVFLPPKPKDLMISRTPEVTCVVVDVSHE 296

QY 301 DPDVQISWVFNVEVHTAQTQTHREDYNTIRVSTLPVHODWMSGKBEKCKVNNKDL 360

Db 297 DPDVQISWVFNVEVHTAQTQTHREDYNTIRVSTLPVHODWMSGKBEKCKVNNKDL 356

QY 361 SPIERTISKIGLVRAPOVYILPPPAEQLSRKDVSLTCLVGFNPGDISVETWSNGHTE 420

Db 357 APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEMESNGOPEN 416

QY 421 NYKDTAPVLDSDGSYFIYKLNKMTSKWEKTSFSCNVRHEGLNHYLTKTISRSPGK 478

Db 417 NYKTPPMLDSDGSFELYSKLTVDKSRMOQGNVFSVSMHEALHNHTOKLSLSLSPGK 474

RESULT 13

US-10-292-088-14

Sequence 14, Application US/10292088

GENERAL INFORMATION:

APPLICANT: BEDIAN, VAHE

APPLICANT: GLADUE, RONALD P.

APPLICANT: CORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 474

[illegible]

179 VSWNSGALTSGVHTFPAPVLSGLSSVTVTPSSNEGTQTYTCNVNDHKPSNTKVDKTV 238
240 EPSGPISTINPCPCKECHKCPAPNLEGGPSYFIPPPNIKDVLMISLTPKVTCTVVVDYSE 299
239 E-----RKC--CVECPCPAPV-AGPSVFLPPPKDLMISRTPEVTCVVVDYSH 287
300 DDPDVQISWFWNNVEVHTAQOTQTHREDYNSTIRVYSTLPQHQDMSGKEPKCKVNNKDL 359
288 EDPEVQFNWYVDGVEVHNAKTTPREEQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGL 347
360 PSPIERTISKGLVRAPOVYILPPPAQLSRKDYSLTCLVVGFPNPGDISVWTSNGHTE 419
348 PAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 407
420 ENYKDTAPVLDSDGSYFYISKLNMKTSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 478
408 NYKTPPMLDSDGSFFLYSLKLTVDKSRMQQGNVTFSCSVNHEALHNHYTKLSLSPGK 466

Search completed: June 18, 2003, 16:48:36
Job time : 59.3933 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: June 18, 2003, 16:44:27 ; Search time 296.065 Seconds
(without alignments)
1040.930 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLLFCLVFFSCVLSQ.....RHEGLKNYLLKKTISRSPGK 478

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
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- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
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- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	2552	100.0	478	21	US-09-770-916-2
2	2083.5	81.6	454	20	US-09-653-755A-4
3	2083.5	81.6	462	20	US-09-653-755A-6
4	2082	81.6	457	21	US-09-791-537-127944
5	2067	81.0	474	21	US-09-791-537-54066
6	2024.5	79.3	475	21	US-09-791-537-126419

7	1802	70.6	336	21	US-09-791-537-26476	Sequence 26476, A
8	1798	70.5	335	21	US-09-791-537-40387	Sequence 40387, A
9	1797	70.4	405	21	US-09-791-537-26475	Sequence 26475, A
10	1793	70.3	404	21	US-09-791-537-40389	Sequence 40389, A
11	1784	69.9	336	21	US-09-791-537-62004	Sequence 62004, A
12	1778	69.7	336	21	US-09-791-537-40377	Sequence 40377, A
13	1751	68.6	468	3	US-07-743-329-7	Sequence 7, Appli
14	1751	68.6	468	7	US-08-303-569-7	Sequence 7, Appli
15	1751	68.6	468	8	US-08-485-686-7	Sequence 7, Appli
16	1751	68.6	468	17	US-09-348-224-7	Sequence 7, Appli
17	1742	68.3	468	12	US-08-846-658A-7	Sequence 7, Appli
18	1742	68.3	468	12	US-08-846-658B-7	Sequence 7, Appli
19	1742	68.3	468	21	US-09-795-515-7	Sequence 7, Appli
20	1739	68.1	446	21	US-09-791-537-12231	Sequence 12231, A
21	1727.5	67.7	469	8	US-08-462-767-2	Sequence 2, Appli
22	1727.5	67.7	469	21	US-09-791-537-126760	Sequence 126760, A
23	1725.5	67.6	444	21	US-09-791-537-87449	Sequence 87449, A
24	1725.5	67.6	461	21	US-09-791-537-28655	Sequence 28655, A
25	1648	64.6	437	21	US-09-791-537-52926	Sequence 52926, A
26	1643	64.4	468	24	US-10-058-120-12	Sequence 12, Appli
27	1596	62.5	476	19	US-09-584-166B-12	Sequence 12, Appli
28	1580.5	61.9	446	20	US-09-618-380-7	Sequence 7, Appli
29	1547.5	60.6	457	21	US-09-791-537-112963	Sequence 7, Appli
30	1528	59.9	470	21	US-09-791-537-56006	Sequence 56006, A
31	1519.5	59.5	472	21	US-09-791-537-29038	Sequence 29038, A
32	1497.5	58.7	464	1	PCT-USQ1-14151-23	Sequence 23, Appli
33	1486	58.2	461	7	US-08-338-503-2	Sequence 2, Appli
34	1486	58.2	444	21	US-09-791-537-34061	Sequence 34061, A
35	1485.5	58.2	444	21	US-08-267-641-18	Sequence 152190, A
36	1484	58.2	599	6	US-08-949-382-18	Sequence 18, Appli
37	1484	58.2	599	13	US-08-480-120-2	Sequence 2, Appli
38	1482	58.1	456	8	US-09-613-017-2	Sequence 2, Appli
39	1472	57.7	456	20	US-09-903-327A-2	Sequence 2, Appli
40	1472	57.7	456	23	US-09-053-583-9	Sequence 9, Appli
41	1472	57.7	464	14	US-09-408-646-9	Sequence 9, Appli
42	1472	57.7	464	18	US-09-499-662-9	Sequence 9, Appli
43	1472	57.7	464	18	US-10-216-484-9	Sequence 9, Appli
44	1472	57.7	464	26	US-09-791-537-89130	Sequence 89130, A
45	1471.5	57.7	458	21		

ALIGNMENTS

RESULT 1

US-09-770-916-2
; Sequence 2, Application US/09770916
; GENERAL INFORMATION:
; APPLICANT: Frank, Dara W.
; APPLICANT: Wiener-Kronish, Jeannine
; APPLICANT: Jahr, Timothy L.
; APPLICANT: Sawa, Teiji
; APPLICANT: Fritz, Robert B.
; TITLE OF INVENTION: Method of and compositions for immunization with the
; FILE REFERENCE: 650053.91487
; CURRENT APPLICATION NUMBER: US/09770,916
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/448,339
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/109,952
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/126,794
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: mouse
US-09-770-916-2

Query Match 100.0%; Score 2552; DB 21; Length 478;


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318 AQTQTHREDYNSTIRVVSFLPIQHODWMSKEFKCKVNKKDLPSPIERTISKIKGLVRAP 377
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294 AQTQTHREDYNSTIRVVSFLPIQHODWMSKEFKCKVNKKDLPSPIERTISKIKGLVRAP 353
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354 QYIILPPPAEQLSRKDVSLTCLVGFNPGDISVEWTSGHTEENYKDTAPVLDSGGSYFI 413
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438 YSKLNMKTSKWEKTDSPFCNVSRHEGLKNYYLKKTISRSPGK 478
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RESULT 4
US-09-791-537-127944
; Sequence 127944, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127944
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-127944

Query Match          81.6%; Score 2082; DB 21; Length 457;
Best Local Similarity 84.3%; Pred. No. 2.4e-161;
Matches 388; Conservative 31; Mismatches 37; Indels 4; Gaps 2;
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; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54066
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-791-537-54066

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; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26475
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-26475

Query Match
Best Local Similarity 100.0%; Score 1797; DB 21; Length 405;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

143 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
1 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
383 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 442
241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 477
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 335

; RESULT 10
; US-09-791-537-40389
; Sequence 40389, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40389
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus musculus
S-09-791-537-40389

Query Match
Best Local Similarity 100.0%; Score 1793; DB 21; Length 404;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

144 KTTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 203
1 KTTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
204 YTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPAP 263
61 YTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPAP 120
264 NLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 323
1 NLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
383 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 442
241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

; RESULT 12
; US-09-791-537-40377
; Sequence 40377, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40377
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-40377

Query Match
Best Local Similarity 100.0%; Score 1784; DB 21; Length 336;
Matches 332; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

143 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
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203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
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181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
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241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

; RESULT 11
; US-09-791-537-62004
; Sequence 62004, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62004
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-62004

Query Match
Best Local Similarity 98.8%; Score 1784; DB 21; Length 336;
Matches 332; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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1 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
383 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 442
241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

; RESULT 10
; US-09-791-537-40389
; Sequence 40389, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40389
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus musculus
S-09-791-537-40389

Query Match
Best Local Similarity 100.0%; Score 1793; DB 21; Length 404;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

144 KTTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 203
1 KTTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
204 YTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPAP 263
61 YTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPAP 120
264 NLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 323
1 NLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
383 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 442
241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336

; RESULT 12
; US-09-791-537-40377
; Sequence 40377, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40377
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-40377

Query Match
Best Local Similarity 100.0%; Score 1784; DB 21; Length 336;
Matches 332; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

143 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 202
1 AKTTPPSVYPLAPGCGDGTGSSVTLGCLVKGYPFESVTVTNWNSGLSSSVHTFPALQSG 60
203 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSPGISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 322
121 PNLEGGPSVFIFFPNKIDVLMISLTPKVTVCVVVDYSEDVQVSWFVNNVEVHTAQOT 180
323 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 382
181 HREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYL 240
383 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 442
241 PPAAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSGSGSYFIYSKLN 300
443 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 478
301 MKTSKWEKTSFSCNVRHEGLKNYLLKTTISRSPG 336
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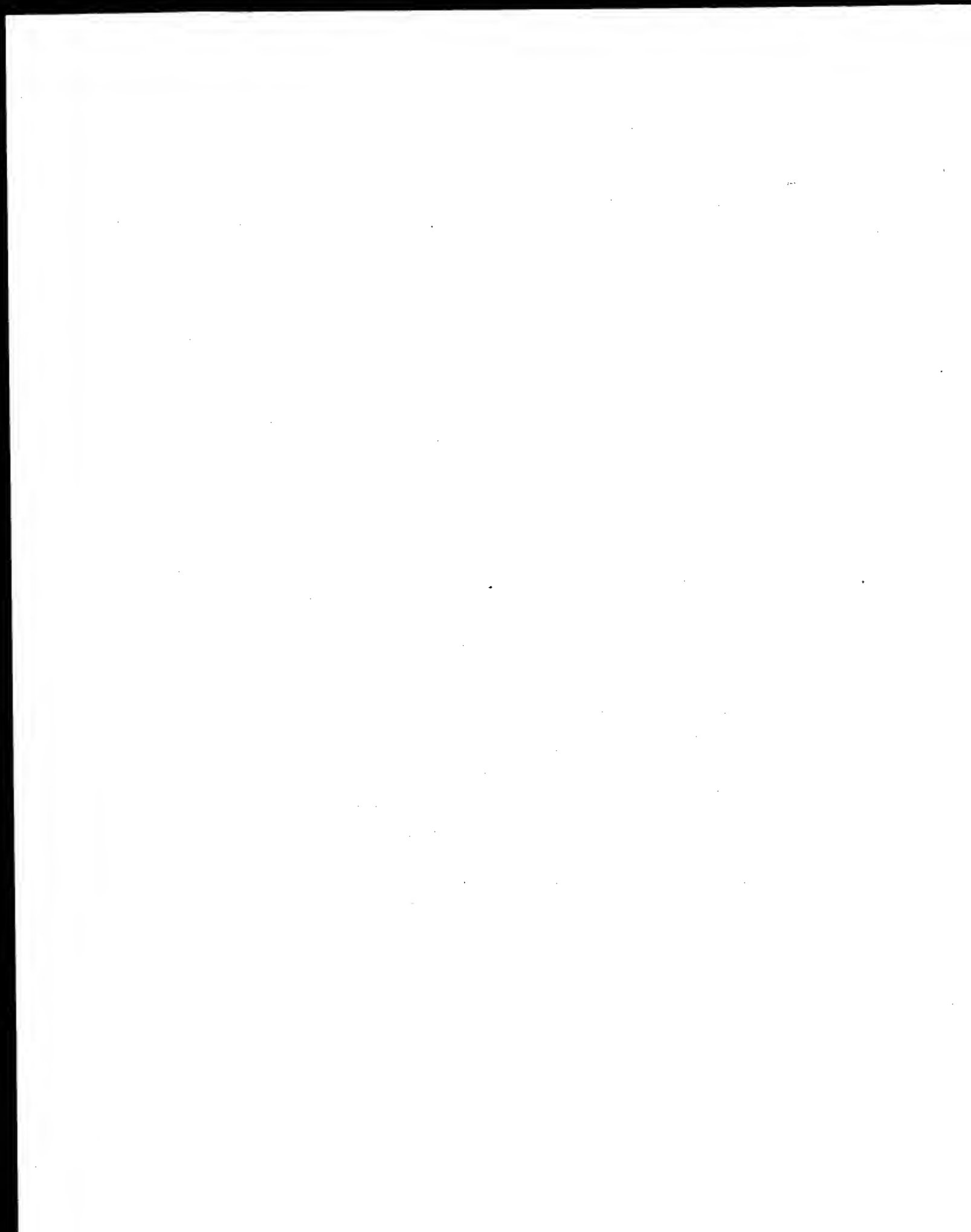
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 40377
LENGTH: 336
TYPE: PRT
ORGANISM: Mus musculus
-09-791-537-40377

Query Match 69.7%; Score 1778; DB 21; Length 336;
Best Local Similarity 98.8%; Pred. No. 1.3e-136;
Matches 332; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
143 AKTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPFESVTVWNSGLSSSVHTFFALLQSG 202
1 AKTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPFEPVTVWNSGLSSSVHTFFALLQSG 60
203 LYTMSSSVTVPSSTWPSQTVCSVAHPASSTVVDKLEPSPGPISTINPCPCKECHKCPA 262
61 LYTMSSSVTVPSSTWPSQTVCSVAHPASSTVVDKLEPSPGPISTINPCPCKECHKCPA 120
263 PNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDVQISWFNVEVHTAQOT 322
121 PNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDVQISWFNVEVHTAQOT 180
323 HREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKGLVRAPOVYL 382
181 HREDYNSTIRVSHLPIQHODWMSGKEFKCKVNNKDLPSPIERTISKGLVRAPOVYL 240
383 PPPAQQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
241 PPPAQQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
443 MKTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 478
301 MKTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 336

RESULT 13
US-09-743-329-7
Sequence 7, Application US/07743329
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,329
FILING DATE: 19910917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: CARP-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-743-329-7
Query Match 68.6%; Score 1751; DB 3; Length 468;
Best Local Similarity 69.0%; Pred. No. 3.3e-134;
Matches 327; Conservative 60; Mismatches 7; Indels 12; Gaps 4;
QY 6 LLFCLVTPPSCVLSQVQLKQSGPGLVQPSQSLISITCTVSGFSLTSGYVHWVRQSPGKLE 65
DB 6 IFLLLSVTAGVHSQVQLQSGAELARPGASVKNSKASGYTFTRYTHMWVQRPGQGLE 65
QY 66 WLGIW-MSGGTDYNAAFISRLSISKDKNSKLSQLPFKMNSLRATDTAIYYCARNRGGDIYD 124
DB 66 WIGYINPSRGVTYNNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYYCAR- ----YD 120
QY 125 FTYAMDYWGQGTSTVTVSSAKTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPFESVTVTN 184
DB 121 DHYCLDYWGQGTSTVTVSSAKTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPFEPVTLTN 180
QY 185 SGLSSSVHTFPALLOSLGLYTMSSSVTVPSSTWPSQTVCSVAHPASSTVVDKLEPSPG 244
DB 181 SGLSSSVHTFPALLOSLGLYTMSSSVTVPSSTWPSQTVCSVAHPASSTVVDKLEPSPG 240
QY 245 1STINPCPCKECHKCPAPNLEGGPSVFIPPNKIDVLMISLTPKVTVCVVVDVSEDDPDV 304
DB 241 --TKPCPC-----KCPAPNLLGGPSVFIPPKIDVLMISLTPKVTVCVVVDVSEDDPDV 294
QY 305 QISWFNVEVHTAQOTHREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKDLPSPIE 364
DB 295 QISWFNVEVHTAQOTHREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKDLPSPIE 354
QY 365 RTISKIGLVRAPQVYILPPPAQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYK 424
DB 355 RTISKIGLVRAPQVYILPPPAQLSRKDVSLTCLVVGPNPGDISVEWTSNGHTEENYK 414
QY 425 TAPVLDSDGSYFIYSKLNKMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 478
DB 415 TEPVLDSDGSYFIYSKLNKMTSKWEKTDSPFCNVRHEGLKNYLLKKTISRSPGK 468

RESULT 14
US-08-303-569-7
Sequence 7, Application US/08303569
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,329
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:46:17 ; Search time 44.9803 Seconds
(without alignments)
1149.899 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLECLVTFPSCVLSQ.....RHEGLKNYLKTKISRPGK 478

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1742	68.3	468	9	US-09-795-515-7
2	1472	57.7	456	9	US-09-903-327A-2
3	1472	57.7	464	9	US-10-216-484-9
4	1458	57.1	451	9	US-10-153-382-17
5	1456.5	57.1	452	9	US-09-726-258-71
6	1452.5	56.9	551	10	US-09-815-837-93
7	1445	56.6	476	9	US-10-124-905-12
8	1445	56.6	476	9	US-09-948-429B-12
9	1440	56.4	451	10	US-09-822-698A-26
10	1439.5	56.4	475	10	US-09-740-002-27
11	1434	56.2	470	9	US-10-020-786-9
12	1434	56.2	470	9	US-10-227-694-5
13	1432	56.1	464	9	US-10-153-382-9
14	1430.5	56.1	450	9	US-09-996-288-220
15	1430.5	56.1	450	9	US-09-996-265-220
16	1430.5	56.1	450	10	US-09-796-848A-37
17	1430.5	56.1	463	9	US-10-153-382-3
18	1430.5	56.1	463	9	US-10-153-382-13
19	1430.5	56.1	475	10	US-09-740-002-25

Sequence 12, Appl
Sequence 36, Appl
Sequence 6, Appl
Sequence 22, App
Sequence 224, App
Sequence 224, App
Sequence 224, App
Sequence 39, Appl
Sequence 41, Appl
Sequence 5, Appl
Sequence 32, Appl
Sequence 232, App
Sequence 234, App
Sequence 236, App
Sequence 232, App
Sequence 234, App
Sequence 236, App
Sequence 2, Appl
Sequence 210, App
Sequence 238, App
Sequence 240, App
Sequence 242, App
Sequence 244, App
Sequence 246, App
Sequence 210, App

ALIGNMENTS

RESULT 1

US-09-795-515-7
; Sequence 7, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

[illegible]

Db 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451

RESULT 5

US-09-726-258-71

; Sequence 71, Application US/09726258

; Publication NO. US20030021790A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hsei, Vanessa

; APPLICANT: Koumenis, Iphigenia

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Shahrokh, Zahra

; APPLICANT: Zapata, Gerardo A.

; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND

; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/726.258

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/234,182

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/094003

; FILING DATE: 24-JUL-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1085R4-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-09-726-258-71

Query Match 57.1%; Score 1456.5; DB 9; Length 452;

Best Local Similarity 60.1%; Pred. No. 5.4e-74;

Matches 277; Conservative 68; Mismatches 105; Indels 11; Gaps 5;

QY 20 OYOLKSGPGLVOPSOQLSTICVSGFSLTSYGVHVRQSPGKLEWLVI-WSGGDTDY 78

Db 1 EVOLVGGGLVQPGGSLRLSCAASGYFSSHYMHVVRQAPGKLEWVGYIDPSNGETTY 60

QY 79 NAAFISSLISKNSKNSQLFFKNSLRATDAIYCCARNRGDIYYDTYAMDYWGQTSV 138

Db 61 NOKFKGRFTLSRDNKNTAYLOHNSLRAEDTAVYYCA--RGDYRYNGDWFDFVWGQTLV 118

QY 139 TVSSAKTTPSVVPLAPGCGDTTGGSSVTGLCLVKGFPPSVTVTNWSSGLSSSVHTFPAL 198

Db 119 TVSSASTKGSFVPLAPSSKSTSGGTAALGLCLVKDYFPEPTVYSWNSGALTSGVHTFPV 178

QY 199 LO-SGLYTTSSSVTVPSSTWSPQSTVTCVSAHPASSTVYDKKLEPSPGPISTINCPCKEC 257

Db 179 LOSSGLYLSUSVTVPSSSGLTQYICNNVHKPNSNTKVDKPKVPSKCDKT-HTCPP---- 233

Tue Jul 1 18:40:53 2003

258 HKCAPNLEGSPSVFPPNPKDVLMSLTPKVTCTVVVDSEDDPDVQISWFYNNVEVHT 317
 234 --CPAPELGGSPSVFPPPKDVLMSLTPKVTCTVVVDSEDDPDVQISWFYNNVEVHT 291
 318 AQTQTHREDYNSTRVSTLPIQHQDMGSKFKCKVNNKDLPSPIERTISKI GLVRAP 377
 292 AKTKPREEQNSYRVSFVTLVHQDLNGKEYCKKVSNNKALPAPTEKTSKAKGQPREP 351
 378 QVYLPPAPQLSRKDVSLTCLVGVNPGDISVETNSNGHTENYKDTAPVLDSDGSYFI 437
 352 QVYTLPPSREEMTKNQVSLTCLVGVNPGDISVETNSNGHTENYKDTAPVLDSDGSFEL 411
 438 YSKLNMKTSKWEKTSFSCNVHGLKNYLYKKTISRSPGK 478
 412 YSKLTVDKSRMOQGNFSCSVHGLHNNHYTKQSLSLSPGK 452

SULT 6
 -09-815-837-93
 Sequence 93, Application US/09815837
 Patent No. US20020082411A1
 GENERAL INFORMATION:
 APPLICANT: Carter, Darrick
 APPLICANT: Zhu, Shirley
 APPLICANT: Arimilli, Subhashini
 APPLICANT: Wang, Aijun
 APPLICANT: Corixa Corporation
 TITLE OF INVENTION: Immune Mediators and Related Methods
 FILE REFERENCE: 014058-00567005
 CURRENT APPLICATION NUMBER: US/09/815,837
 CURRENT FILING DATE: 2001-03-22
 PRIOR APPLICATION NUMBER: US 60/191,274
 PRIOR FILING DATE: 2000-03-22
 PRIOR APPLICATION NUMBER: US 60/204,249
 PRIOR FILING DATE: 2000-05-15
 PRIOR APPLICATION NUMBER: US 60/264,003
 PRIOR FILING DATE: 2001-01-23
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 93
 LENGTH: 551
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: pCB223
 OTHER INFORMATION: recombinant MHC class II heterodimer
 -09-815-837-93

Query Match 56.9%; Score 1452.5; DB 10; Length 551;
 Best Local Similarity 62.4%; Pred. No. 1.le-73;
 Matches 289; Conservative 48; Mismatches 71; Indels 55; Gaps 9;
 30 LVQPSQSLISITCTVSGFSLTSYGVHVRQSPGKLEGLVWISGDDTDYNAFISRLSIS 89
 130 LCQPN--TLICFVDNIPFPVINITWLRNSK-----SVTDGVVETSF--VN 171
 90 KDNKSKQLFFKMSNLUR--ATDTAIIYCAARNRGGDIYDFTYANDYWGQTSV----- 138
 172 RDHS----FKLSYLTFTIPSDDDIYDC-----KVEHWGLEEPLVKKHWEPEIP 214
 139 ---TVSSAKTTPPSVYVPLAPGCGDTGSSVTLGCLVKGYEPESVTVWNSGSLSSVHTF 195
 215 APMSEGSAKTTPSYPVPLAPGCGDTGSSVTLGCLVKGYEPESVTVWNSGSLSSVHTF 274
 196 PALLOGLTVMSSVTVPSSTVQVTCVSAHPASSTVVDKLEPSPGPISTINPCPPCK 255
 275 PAVLQSDLYTLSSSVTVTSWPSQITCNVAHPASSTVVDKLEPSPGPISTINPCPPCK 331
 256 ECHKCAPNLEGSPSVFIPPPNPKDVLMSLTPKVTCTVVVDSEDDPDVQISWFYNNVEV 315
 332 ---KCPAPNLEGSPSVFIPPPNPKDVLMSLTPKVTCTVVVDSEDDPDVQISWFYNNVEV 388
 316 HTAQQTQTHREDYNSTRVSTLPIQHQDMGSKFKCKVNNKDLPSPIERTISKI GLVR 375

Db 389 HTAQQTQTHREDYNSTRVSTLPIQHQDMGSKFKCKVNNKDLPSPIERTISKI PKGSVR 448
 QY 376 APOVYILPPAPQLSRKDVSLTCLVGVNPGDISVETNSNGHTENYKDTAPVLDSDGSY 435
 Db 449 APOVYVLPPEEEMTKQVTLTCTVTDMPEDIVYVETNNGKTELNYKNTPEVLDSDGSY 508
 QY 436 FIYSKLNKMTSKWEKTSFSCNVHGLKNYLYKKTISRSPGK 478
 Db 509 FMYSKLVRKKNVVERNSYSCSVVHGLHNNHYTKQSLSLSPGK 551

RESULT 7
 US-10-124-905-12
 ; Sequence 12, Application US/10124905
 ; Patent No. US20020166136A1

GENERAL INFORMATION:
 APPLICANT: Anderson, Darrell R.
 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/124,905
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/383,916
 FILING DATE:
 APPLICATION NUMBER: US 08/487,550
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-10-124-905-12

Query Match 56.6%; Score 1445; DB 9; Length 476;
 Best Local Similarity 57.8%; Pred. No. 2.5e-73;
 Matches 281; Conservative 72; Mismatches 115; Indels 18; Gaps 7;
 QY 1 MAVIGLLFCVLTFPPSCVLSQVQLKQSGPGLVQPSQSLISITCTVSGFSLT-SYGVHVRQS 59
 Db 1 MKHLFFLLVLAAPRWLSQVQLKQSGPGLVQPSQSLISITCTVSGFSLT-SYGVHVRQS 60
 QY 60 PKGKLEWLGVIW-SGGDDTDYNAFISRLSISKDNKSKQLFFKMSNLURATDIYICARNR 118
 Db 61 PKGKLEWISGFYSSSGNTYINPFLSKQVITSTDTSKNQFSLKNSMTAADTAVYICVRDR 120
 QY 119 -----GDIYDFTYANDYWGQTSVTSVSAKTTTPPSVYVPLAPGCGDTTGSVTLGCLVK 173

Db 121 LFSVGMVYNNW---FDVWPGVLVTSSASTKGPVFLAPSSKSTSGTAALGCLVKD 177
QY 174 YPESVYVWNSGSLSSSVHTTPALQ-SGLYTMSSSVTPSPSTWPSQTWTCVAHPASS 232
Db 178 YPEPVTVWNSGALTSVHTTPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHPKN 237
QY 233 TVVDKLEPSPISINCPCKCKCHKCPAPNLEGPSVFIPPNKIDVLMISLTPKVTC 292
Db 238 TKVDKAEKPKCDKT-HTCPCP-----CPAPELGGPSVFLFPKPKDTLMISRTPEVC 290
QY 293 VVDYSEDDPDVQISWFWNNVHTAQTOTHRDYNSTIRVYSTLPQIHOHDMGSKFKC 352
Db 291 VVDYSHEDPEVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKEYKC 350
QY 353 KVNKDLPSPIERTISKIKGLVRAPQVYILPPAPQLSRKQVSLTCLVVGPNQDISVEW 412
Db 351 KVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVEW 410
QY 413 TSNHTEENYKDTAPVLDSDGSYFYTKLNKMTSKWEKTDSCNVRHGLKNYLLKTI 472
Db 411 ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSL 470
QY 473 SRSPGK 478
Db 471 SLSPGK 476

RESULT 8

JS-09-948-429B-12
; Sequence 12, Application US/09948429B
; Patent No. US2002017689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-09-948-429B-12

Query Match

56.6%; Score 1445; DB 9; Length 476;

Best Local Similarity 57.8%; Pred. No. 2.5e-73;

Matches 281; Conservative 72; Mismatches 115; Indels 18; Gaps 7;

QY 1 MAVLGLFLCFLVFPSCVLSQVQLKQSGPGLVQPQSLISITCTVSGFSLT-SYGVHVVWROS 59
Db 1 MKHLWFLLLVAAAPRWLVLSQVQLQESGPGLVKPELTLTCAVSGGSISGGYGMWIRQP 60
QY 60 PKGKLEWLGVW-SGGDTYDAAFIARLSISKDNKSQSLFFKMNLSRATDAIYYCARNR 118
Db 61 PKGLEWIGSFYSSSGNTYVNPSSKQVITSTDTKSNQSLKLSNMTAATAVYVCVRDR 120
QY 119 -----GDIIYDFTYAMDYCOGTSVTVSSAKTTPPSVYPLAPCGDITGSSVTLGLVK 173
Db 121 LFSVGMVYNNW---FDVWPGVLVTSSASTKGPVFLAPSSKSTSGTAALGCLVKD 177
QY 174 YPESVYVWNSGSLSSSVHTTPALQ-SGLYTMSSSVTPSPSTWPSQTWTCVAHPASS 232
Db 178 YPEPVTVWNSGALTSVHTTPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHPKN 237
QY 233 TVVDKLEPSPISINCPCKCKCHKCPAPNLEGPSVFIPPNKIDVLMISLTPKVTC 292
Db 238 TKVDKAEKPKCDKT-HTCPCP-----CPAPELGGPSVFLFPKPKDTLMISRTPEVC 290
QY 293 VVDYSEDDPDVQISWFWNNVHTAQTOTHRDYNSTIRVYSTLPQIHOHDMGSKFKC 352
Db 291 VVDYSHEDPEVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVLTVLHODWLNKEYKC 350
QY 353 KVNKDLPSPIERTISKIKGLVRAPQVYILPPAPQLSRKQVSLTCLVVGPNQDISVEW 412
Db 351 KVSNKALPAPIEKTISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFPYPSDIAVEW 410
QY 413 TSNHTEENYKDTAPVLDSDGSYFYTKLNKMTSKWEKTDSCNVRHGLKNYLLKTI 472
Db 411 ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSL 470
QY 473 SRSPGK 478
Db 471 SLSPGK 476

RESULT 9

US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin heavy chain of MUC1-specific PH1-IgG1
US-09-822-698A-26

Query Match 56.4%; Score 1440; DB 10; Length 451;

Best Local Similarity 59.9%; Pred. No. 4.5e-73;

Matches 276; Conservative 67; Mismatches 106; Indels 12; Gaps 5;

QY 20 QVQLKQSGPGLVQPQSLISITCTVSGFSLTSYGVHVVWROSQSPKGLWLG-VVIWSGGDTDY 78
Db 1 QVQLVQSGGGLVQPQGGSLRLSCAASGFTFRSNMGWVRQAPKGLWVSGISGGSGTY 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:42:37 ; Search time 23.4972 Seconds
(without alignments)
598.546 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVLGLLFCLVTFPSCVLSQ.....RHEGLKNYLYKTKTSRSPQK 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUTS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1751	68.6	468	2	US-08-116-247-7
2	1742	68.3	468	2	US-08-303-569B-7
3	1580.5	61.9	446	3	US-08-397-411-7
4	1515	59.4	464	1	US-08-353-400-36
5	1506	59.0	445	1	US-08-353-400-33
6	1484	58.2	599	1	US-08-442-542-18
7	1484	58.2	599	3	US-08-765-469-18
8	1471.5	57.7	473	4	US-09-049-672A-4
9	1460	57.2	447	6	5455030-1
10	1456.5	57.1	452	3	US-09-027-449-71
11	1456.5	57.1	452	4	US-09-026-985-71
12	1456.5	57.1	452	4	US-09-121-952A-71
13	1456.5	57.1	452	4	US-09-234-340A-71
14	1445	56.6	476	3	US-08-487-550-12
15	1429.5	56.0	467	4	US-08-523-894-12
16	1428	56.0	472	4	US-08-793-450-8
17	1422.5	55.7	449	4	US-09-679-397-2
18	1422.5	55.7	449	4	US-09-680-148-2
19	1422.5	55.7	467	4	US-08-523-894-10
20	1422	55.7	451	2	US-08-887-352B-14
21	1422	55.7	451	2	US-08-887-352B-16
22	1422	55.7	451	2	US-08-887-352B-18
23	1422	55.7	451	3	US-08-466-151-65
24	1422	55.7	451	4	US-09-109-207C-14
25	1422	55.7	451	4	US-09-109-207C-16
26	1422	55.7	451	4	US-09-109-207C-18
27	1422	55.7	451	4	US-09-282-505-2

28	1422	55.7	451	4	US-09-054-255-2	Sequence 2, Appli
29	1422	55.7	451	4	US-09-296-005-14	Sequence 14, Appl
30	1422	55.7	451	4	US-09-296-005-16	Sequence 16, Appl
31	1422	55.7	451	4	US-09-296-005-18	Sequence 18, Appl
32	1416	55.5	476	3	US-08-487-550-4	Sequence 4, Appli
33	1414.5	55.4	467	4	US-08-523-894-8	Sequence 8, Appli
34	1405	55.1	443	5	PCT-US96-13152-4	Sequence 4, Appli
35	1404.5	55.0	467	1	US-08-704-744-81	Sequence 81, Appl
36	1403	55.0	467	4	US-09-049-672A-8	Sequence 8, Appli
37	1401	54.9	472	4	US-09-301-593-30	Sequence 30, Appl
38	1400.5	54.9	453	4	US-09-301-593-18	Sequence 18, Appl
39	1400.5	54.9	469	2	US-07-934-373C-23	Sequence 23, Appl
40	1400.5	54.9	469	3	US-08-437-642B-23	Sequence 23, Appl
41	1400.5	54.9	469	4	US-08-146-206C-23	Sequence 23, Appl
42	1400	54.9	453	3	US-08-466-151-8	Sequence 8, Appli
43	1400	54.9	453	4	US-08-466-163B-8	Sequence 8, Appli
44	1399.5	54.8	459	1	US-08-157-101A-7	Sequence 7, Appli
45	1399.5	54.8	552	5	PCT-US93-07832-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-116-247-7
; Sequence 7, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Ahwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-247-7

Query Match 68.6%; Score 1751; DB 2; Length 468;
Best Local Similarity 69.0%; Pred. No. 3.6e-132;
Matches 327; Conservative 60; Mismatches 75; Indels 12; Gaps 4;
QY 6 LLFCLVFPSCVLSQVQLKQSGPGLVPSQSLSTICTVSGFSLTSYGVHWRSPGKGLG 65

6 IFLLLSVTAGVHQSQVQLQSGAELARPGASVKMSCKASGYTFYRTHHWVKQRPGQGLE 65
66 WLGYI-WSGGDTYNAAFISRLSTKDNKSKQLFFKMNLSRATDTAIYICARNRDIYD 124
66 WIGYINPSRGVTNYNQKFKDKATLTIDKSSSTAYMQLSSLTSEDSAVYYCAR-----YYD 120
125 FTYANDYWGQGTSTVTSNAKTTTPPSVYPLAPCGDGTGSSVTLGCLVKGYRPPESVTVTN 184
121 DRYCLDYWGQGTTLTVSSAKTAPSVYPLAPVCGDGTGSSVTLGCLVKGYRPPVTLTN 180
185 SGLSSSVHTFPALLQSLGYTMSSSVTVPSSTWPSQITCNVAHPASSTVDKLEPSP 244
181 SGLSSSVHTFPALLQSLGYTMSSSVTVPSSTWPSQITCNVAHPASSTVDKLEPSP 240
245 ISTINPCPCCKECHKCAPNLEGSPSVIFPPNPKIDVLMISLTPKVTCTVVDVSEDDPDV 304
241 --TIKPCPC---KCAPNLLGGSPSVIFPPNPKIDVLMISLTPKVTCTVVDVSEDDPDV 294
305 QISWVNNVEVHTAQTHREDYNSTIRVWSTLPIQHDQWMSGKFEKCKVNNKDLPSPIE 364
295 QISWVNNVEVHTAQTHREDYNSTIRVWSTLPIQHDQWMSGKFEKCKVNNKDLPSPIE 354
365 RTISKIKGLVRAPQVYLLPAPAEQLSRKDVSLTCLVGVGNPGDISVETNSNGHTENYKD 424
355 RTISKPKGSVRAPQVYLLPAPAEQLSRKDVSLTCLVGVGNPGDISVETNSNGHTENYKD 414
425 TAPVLDSGSGFYIYSKLNKMTSKWEKTSFSCNVRHGLKNYLYKKTISRSPGK 478
415 TEPVLDSGSGFYIYSKLNKMTSKWEKTSFSCNVRHGLKNYLYKKTISRSPGK 468

RESULT 2

3-08-303-569B-7
Sequence 7, Application US/08303569B
Patent No. 5859205
GENERAL INFORMATION:
APPLICANT: Agair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569B
FILING DATE: 07-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-303-569B-7

Query Match 68.3%; Score 1742; DB 2; Length 468;
Best Local Similarity 68.8%; Pred. No. 1.9e-131;
Matches 326; Conservative 60; Mismatches 70; Indels 12; Gaps 4;
6 LLFCLVTPPSCVLSQVQLKQSGPGLVQPQSLSITCTVSGFSLTSGYGVHWKQSPGKLE 65
6 IFLLLSVTAGVHQSQVQLQSGAELARPGASVKMSCKASGYTFYRTHHWVKQRPGQGLE 65
66 WLGYI-WSGGDTYNAAFISRLSTKDNKSKQLFFKMNLSRATDTAIYICARNRDIYD 124
66 WIGYINPSRGVTNYNQKFKDKATLTIDKSSSTAYMQLSSLTSEDSAVYYCAR-----YYD 120
125 FTYANDYWGQGTSTVTSNAKTTTPPSVYPLAPCGDGTGSSVTLGCLVKGYRPPESVTVTN 184
121 DRYCLDYWGQGTTLTVSSAKTAPSVYPLAPVCGDGTGSSVTLGCLVKGYRPPVTLTN 180
185 SGLSSSVHTFPALLQSLGYTMSSSVTVPSSTWPSQITCNVAHPASSTVDKLEPSP 244
181 SGLSSSVHTFPALLQSLGYTMSSSVTVPSSTWPSQITCNVAHPASSTVDKLEPSP 240
245 ISTINPCPCCKECHKCAPNLEGSPSVIFPPNPKIDVLMISLTPKVTCTVVDVSEDDPDV 304
241 --TIKPCPC---KCAPNLLGGSPSVIFPPNPKIDVLMISLTPKVTCTVVDVSEDDPDV 294
305 QISWVNNVEVHTAQTHREDYNSTIRVWSTLPIQHDQWMSGKFEKCKVNNKDLPSPIE 364
295 QISWVNNVEVHTAQTHREDYNSTIRVWSTLPIQHDQWMSGKFEKCKVNNKDLPSPIE 354
365 RTISKIKGLVRAPQVYLLPAPAEQLSRKDVSLTCLVGVGNPGDISVETNSNGHTENYKD 424
355 RTISKPKGSVRAPQVYLLPAPAEQLSRKDVSLTCLVGVGNPGDISVETNSNGHTENYKD 414
425 TAPVLDSGSGFYIYSKLNKMTSKWEKTSFSCNVRHGLKNYLYKKTISRSPGK 478
415 TEPVLDSGSGFYIYSKLNKMTSKWEKTSFSCNVRHGLKNYLYKKTISRSPGK 468

RESULT 3

US-08-397-411-7
Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-411-7

```

Query Match	61.9%;	Score 1580.5;	DB 3;	Length 446;
Best Local Similarity	64.6%;	Pred. No. 1.5e-118;		
Matches 297; Conservative	63;	Mismatches 85;	Indels 15;	

```

20  QVQKQSGPGLVDPQSLSITCTVSGFSLTSYGVHWYRQSPGKGLEWLGIWMSGDTDYN  79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  QVQLQESGPLVKRPSETLSTCTVSGFSLTSYGVHWYRQSPGKGLEWIGVKWSGGSTEYN  60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80  AAFISRLSIKDNKSKSQLEFKMNSLRATDAIYYCAENRGDIIYYDFYIANDYWGQGTSVT  139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61  AAFISRLTISKSDTKNQSIVLKLNSLTAAATYAYICARN-----RYANDYWGQGTFLT  113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
140 VSSAKTTPPVSYYPLAPGCGDPTGSSVTLGCLVKRGFPESVTVTWNSGSLSSSVHTFPALL  199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
114 VSSASTKGPVSFVLAPSSKSTSGTGAALGCLVKDYPPETVTVSNWNGALLSGVHTFPAVL  173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
200 Q-SGLYITMSSSVTPBSSTWFSQIVTCSVAHPASSTVYDKKLFSGPISTINPCPPCKECH  258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
174 QSGGLSLSVTVTPSSSLGTQYICNVNKKPSTKVYDKKVEPKSCDKT--HTCPP-----  227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
259 KCPAPNLEGPSYFIFPPNIKIDVLMISLTPKVTCVVVDSEDDPDQVQISFWFNVEVHTA  318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
228 -CPAPELLGSPSVLEFPKPKDTLMISRPETVTCVVVDVSHEDPEVFKNWIVDGEVEVHNA  286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
319 QTOQTHREDYNSTRVYSTLP IQHQQMWSKEFKCKVNNKDLPSPIERTISKIKGLVRAPO  378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
287 KTAPEEQYNSTRVVSVLTVLHQDLWNGKEYCKYKSNKALPAPIEKTISKAKGQPREPQ  346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
379 VYLLPAPAQLSRKDYSLCTLVVGFNPGDIVSEWNTSGHTEENYKDTAPVLDSDGSYFIY  438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
347 VYTLPSRDELTKNQVSLCTLVKGFYPSDIANWESNGQPENNYKTPPVLDSDGSFFLY  406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
439 SKLNMTKWEKTDSPSCNVRHGLKNYYLKKTIISRPCK  478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 SKLTVDKRWQOQGNFSCSVMHEALHNHYTKQSLSLSPGK  446
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

SUBMIT 4
-08-353-400-36
Sequence 36, Application US/08353400
Patent No. 566537
GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 37
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/353,400
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9324819.3
 FILING DATE: 03-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9411089.7
 FILING DATE: 03-JUN-1994
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:

```

; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-36

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Query Match	59.4%;	Score	1515;	DB 1;	Length	464;	
Best Local Similarity	60.3%;	Pred. No.	2.7e-113;				
Matches	286;	Conservative	72;	Mismatches	100;	Indels	1

	QY	6	LLFCVLTPPSCVLSOVQLKQSGPGVLVPQSOSLSTITCTVSFGSITSUTSVGHWVRSPQKGLE	65
	Db	6	IILFLVATGTVDHVSQVLQQQPAGELVFPGASVOLSKASCAGYTFTGYIHWVKORPQGULE	65
	QY	66	WLG-VIWSGGDIDYNAAFISLSTISKDNKSOLFCKMNSLRATDTATLYCARNRGDIYD	124
	Db	66	WIGEVNPTGSRSDYNEXFKNKATILYDKSSTAYMQLSLTSSEDSAVYYCARERA---	YG 122
	QY	125	FITYAMDYWGQGSTVTVSAAKTTPPSVPLAPGCCGDTTGSSTVLGCCLKVGYPFESVTVTN	184
	Db	123	YDDAMDYWGQGSTVTVSAAKTTPSVYPLAPGSAOQNSMVTLCGLCVKYGFPEPVTVTN	182
	QY	185	SGSLSSSVHTFPALLQGLTYLMSSSNVTPSSTWPSTVTCVSAHPASSITVDKKLEPSP	244
	Db	183	SGSLSSGVHTFPVAVLQSDLTYLSSSVTPSSTWPSETVCNVAHPASSTKVDKIIV--	239
	QY	245	ISTINPCPPCKECHKCAPNLGGPSVFIFFPNIKDVLMISLTPTKVTCVVWDVSEDDPV	304
	Db	240	---RDC-GCKPC-ICTVPEVS---SVFIFFPKPKDVLITLTPKVTCVVVISKDDREV	290
	QY	305	QISNFVNNVVEHTTAQTOTHREDYNSITRVYSTLIPIHQDWMSGKEPKKVNKNKDLPSP	364
	Db	291	QFSWFVDDEVHTTAQTOPREQENSFISRSSELPIMHQDLWLNGKEFKKRVNSAAPPATIE	350
	QY	365	RTISKIRGLRAPOVYILPPPAPQLSRKDVSLVCLVGVGNPDGISVENTNSGHTKENK	424
	Db	351	KTISKTKGRPKAPOVYTI PPPKQMADKVS LCTMTDFEPEDITEVQWNQCPAENTKN	410
	QY	425	TAPVLDSGDSFYFYISKLNWKTSKWEKTDSEFSONVRHEGLKNXYLKKTISRSPGK	478
	Db	411	TQPMTDGTDSFYFYKLVNOKSWNEAGNTFTCSVLHEGLHNHHTEKLSHSHPGK	464

REPORT 5
 US-08-353-400-33
 : Sequence 33, Application US/08353400
 : Patent No. 5665357
 : GENERAL INFORMATION:
 : APPLICANT:
 : TITLE OF INVENTION: PROTEINS
 : NUMBER OF SEQUENCES: 37
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0,
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/353.400
 : FILING DATE:
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9324819.3
 : FILING DATE: 03-DEC-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9411089.7
 : FILING DATE: 03-JUN-1994
 : INFORMATION FOR SEQ ID NO: 33:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 445 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear

[illegible]

RESULT 8
S-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCUT01
CLONE: 1513264
S-09-049-672A-4

[illegible]


```

RESULT 11
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

Query Match 57.1%; Score 1456.5; DB 4; Length 452;
Best Local Similarity 60.1%; Pred. No. 1.2e-108;
Matches 277; Conservative 68; Mismatches 105; Indels 11; Gaps 5;

y 20 QVOLKQSGGLVQPSQSLITCVSGFSLTSGVGHVWQSPCKGLEWLGVI-WSGGDTDY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 1 EYVLVQSGGGLVQPGGSLRSLSCAAGSYFSSHMHVWVROAPCKGLEWVGVIIDPSNGETTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 79 NAAFTSLRLSKIDNSKQSLFFKNNLSLRATDTAIYCCARNRGDIYDYFTYAMDYWGQGTSV 138
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 61 NOKFKGRFTLRSDNSKNTAYLQMNLSRAEDTAVYYCA--RGDYRYNGDWFFDVGWQGTIV 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 139 TVSSAKTTPPSVYPLAPGGDTGTSVTLGCLVKGYPFESVTVTWNSGLSSSVHTFPAL 198
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 119 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 178
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 199 LQ-SGLYTMSSSVTPSWTSQVTCVSAHPASTTVDDKKLEPSGPISITINPCPPCKEC 257
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 179 LQSSGLYLSVSVTVPSSSLGTTQTVICNVNHPKSNTKYDKKVEPKSCDKT-HTCPP---- 233
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 258 HRCAPAPNLGGPSVFIFPPNKLIVLMI SLTPKVCIVVDVSEDDPDQVQISWVNNVEVHT 317
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 234 --CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVGVHN 291
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 318 AQTQTHREDYNSTIRVSTLPIQHDMMNSGKFEKCKVNNKDLPSPIERTISKIKGLVRAP 377
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
b 292 AKTKPREQYNSYRVSVLTVLHQDLWNGKEYCKVSKNALPAPIEKTISKAGQPREP 351
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y 378 QVYILPPPAEQLSRKDVSITCLVGVGFNPEDTISVETWNSNGHTTEENYKDTAPVLDSGYSFI 437
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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199 LO-SGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKLEPSGPISTINPCPCCKEC 257
179 LOSGLYSLSSVTPSPSSLTGTQYICNVNHPKNTKVKVPEKSCDKT-HTCPCP----- 233
258 HKCAPNLEGGPSVFIFPPNKKVIMSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEVHT 317
234 --CPAPPELLGGPSVFLFPKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHN 291
318 AQTQTHREDYNSTRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
292 AKTPREQYNSTRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREP 351
378 QVYTLPPAEOLSKRDKVSLCLVGVFNPGDISVEWTSNGHTEENYKDTAPVIDSDGSYFI 437
352 QVYTLPPSREMTKNQVSLTCLVKGFPSPDSIAVWESNGQPENNYKTPPPVLDSDGSFFL 411
438 YSKLNMKTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 478
412 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQKLSLSPGK 452

SULT 13

-09-234-340A-71

Sequence 71, Application US/09234340A

Patent No. 6468532

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsai, Vanessa

APPLICANT: Koumenis, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Shahrokh, Zahra

APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES

TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinFatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/234,340A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/121,952

FILING DATE: 24-Jul-1998

APPLICATION NUMBER: 60/074330

FILING DATE: 22-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/075467

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R4

TELEPHONE: 650/225-5530

TELEPHONE: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

S-09-234-340A-71

Query Match 57.18; Score 1456.5; DB 4; Length 452;
Best Local Similarity 60.18; Pred. No. 1.2e-108;
Matches 277; Conservative 68; Mismatches 105; Indels 11; Gaps 5;

QY 20 QVLLKQSGPLVQPSQSLSTICTVSGFSLVGVHVRQSPGKLEWLVGI-WSGGDTDY 78
Db 1 EVLVQSGGGLVQPGGSLRLSCAASGYFSFHHYHVRQAPGKLEWVGIDPSNGETTY 60
QY 79 NAAFIISRLSISKDSKQSLFFKMNLSRATDTAIYYCARNRDIYYDYFYAMDYWGQGTSV 138
Db 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDTAVIYCA--RGDIRYNGDFDFVWGQGTFLV 118
QY 139 TVSSAKTTPPVVYPLAGCGDTTGTSSVTGLCLVKGYPSPESVTVTWNSGLSSSVHTFPAL 198
Db 119 TVSSASTKGPVFLAPSSKSTSGTALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAL 178
QY 199 LO-SGLYTMSSSVTPSPSTWPSQVTCVAHPASSTTVDDKLEPSGPISTINPCPCCKEC 257
Db 179 LOSGLYSLSSVTPSPSSLTGTQYICNVNHPKNTKVKVPEKSCDKT-HTCPCP----- 233
QY 258 HKCAPNLEGGPSVFIFPPNKKVIMSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEVHT 317
Db 234 --CPAPPELLGGPSVFLFPKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHN 291
QY 318 AQTQTHREDYNSTRVSTLPIQHDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
Db 292 AKTPREQYNSTRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREP 351
QY 378 QVYTLPPAEOLSKRDKVSLTCLVGVFNPGDISVEWTSNGHTEENYKDTAPVIDSDGSYFI 437
Db 352 QVYTLPPSREMTKNQVSLTCLVKGFPSPDSIAVWESNGQPENNYKTPPPVLDSDGSFFL 411
QY 438 YSKLNMKTSKWEKTDSCNVRHGLKNYLLKKTISRSPGK 478
Db 412 YSKLTVDKSRWQOGNVFSCSVNHEALHNHYTKQKLSLSPGK 452

RESULT 14

US-08-487-550-12

Sequence 12, Application US/08487550

Patent No. 6113898

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELEPHONE: 703-836-6620

TELEPHONE: 703-836-6620

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-12

Query Match 56.6%; Score 1445; DB 3; Length 476;
Best Local Similarity 57.8%; Pred. No. 1.1e-107;
Matches 281; Conservative 72; Mismatches 115; Indels 18; Gaps 7;
QY 1 MAVLGILLCVLPFPSCVLSQVQLKQSGPGLVPSQSLSTICTVSGFSLT-SYGVHVRQS 59
Db 1 MKHLWFFLLVAAPRWLVLSQVQLKQSGPGLVPSQSLSTICTVSGFSLTCAVSGSGISGGYWGWIROP 60
QY 60 PKGLEWLGVIW-SGGDDTDYNAAFISRLSISKDNKSQSLFFKMNLSLRATDTAIYICARNR 118
Db 61 PKGLEWIGISFYSSGNTYINPISLQVITSDTSKNQFSLKNSMTAADTAVYICVDR 120
QY 119 -----GDIYDFTYAMDYWGQTSVTVSSAKTTPPSVYPLAPCGDGTGSSVTLGCLVKG 173
Db 121 LFSVVGMYNNW---FDVWGPGVLTVSSASTKGPSPVPLAPSSKSTSGGTAALGCLVKD 177
QY 174 YPESVTVTWNSGLSSSVHTFPALLO-SGLYTMSSSVTPSPSTWPSQVNTCSVAHPASS 232
Db 178 YPEPTVSWNSGALTSGVHTFPALVQSSGLYLSVSVTVPSSSLGTQYICNVNHPKN 237
QY 233 TVDKKLEPSPGISTINCPCKCKECHKCPAPNLEGPSVFIFPPNLIKDVLSLTPKVT 292
Db 238 TKVDAKAEPKSCKDT-HTCPP-----CPAPELGPGSVFLFPKPKDPLMISRTPEVTC 290
QY 293 VVVDVSEDDPVOISWFNVNVEVHTAQTQTHREDYNSTIRVYSTLPIDHQDMSGKEFKC 352
Db 291 VVVDVSHEDPEVKFNWYDGVGEVHNNAKTPREEQYNSIYRVVSVLTVLHQDLNKGK 350
QY 353 KVNKDLPSPIERTISKIKGLVRAPQVYILPPAPQLSKDKVSLTCLVVGFPNPGDISVEW 412
Db 351 KVSNNALPAPIEKTIKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW 410
QY 413 TSNGHTEENYKDTAPVLDSDGSFYIYKLNKMTSKWEKTDSECNVRHEGLKNYLLKTI 472
Db 411 ESNQOPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQGNVFSVMEALHNHYTQKSL 470
QY 473 SRSPCK 478
Db 471 SLSPCK 476

RESULT 15

US-08-523-894-12
Sequence 12, Application US/08523894
Patent No. 6136310

GENERAL INFORMATION:

APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-12

Query Match 56.0%; Score 1429.5; DB 4; Length 467;
Best Local Similarity 57.9%; Pred. No. 1.8e-106;
Matches 279; Conservative 74; Mismatches 110; Indels 19; Gaps 7;
QY 1 MAVLGILLCVLPFPSCVLSQVQLKQSGPGLVPSQSLSTICTVSGFSLT-SYGVHVRQS 59
Db 1 MKHLWFFLLVAAPRWLVLSQVQLKQSGPGLVPSQSLSTICTVSGFSLTCAVSGSGISGGYWGWIROP 60
QY 60 PKGLEWLGVIW-SGGDDTDYNAAFISRLSISKDNKSQSLFFKMNLSLRATDTAIYICARNR 118
Db 61 PKGLEWIGIYIYSGGGTNYNPSLNRSISIDTSKNLFSKLRSVTAADTAVYICASN- 119
QY 119 GDIYDFTYAMDYWGQTSVTVSSAKTTPPSVYPLAPCGDGTGSSVTLGCLVKGYPES 178
Db 120 ---ILKYLHLLWYGCGLVTVSSASTKGPSPVPLAPCSRSTSESTAALGCLVKDYFPEP 176
QY 179 VTVWNSGLSSSVHTFPALLO-SGLYTMSSSVTPSPSTWPSQVNTCSVAHPASSITVDK 237
Db 177 VTVWNSGALTSGVHTFPALVQSSGLYLSVSVTVPSSSLGTQYICNVNHPKN 236
QY 238 KLEPS-GPISTINCPCKCKECHKCPAPNLEGPSVFIFPPNLIKDVLSLTPKVTGVVD 296
Db 237 RVESKYGP-----PCPP-----CPAPEGEGPSVFLFPKPKDPLMISRTPEVTCVVD 285
QY 297 VSEDDPVOISWFNVNVEVHTAQTQTHREDYNSTIRVYSTLPIDHQDMSGKEFKCKVNN 356
Db 286 VSEDDPEVQFNWYDGVGEVHNNAKTPREEQYNSIYRVVSVLTVLHQDLNKGKCKVSN 345
QY 357 KDLPSPIERTISKIKGLVRAPQVYILPPAPQLSKDKVSLTCLVVGFPNPGDISVEWTSNG 416
Db 346 KGLPSIEKTIKAKGQPREQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNG 405
QY 417 HTEENYKDTAPVLDSDGSFYIYKLNKMTSKWEKTDSECNVRHEGLKNYLLKTIISRSP 476
Db 406 OPENNYKTPPVLDSDGSFFLYSLRSLVDKSRWQGNVFSVMEALHNHYTQKSLSL 465
QY 477 GK 478
Db 466 GK 467

Search completed: June 18, 2003, 16:49:18
Job time : 25.4972 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:53 ; Search time 65.7921 Seconds
(without alignments)
968.107 Million cell updates/sec

Title: US-09-770-916-2

Perfect score: 2552

Sequence: 1 MAVGLLLCLVFFPSCVLSQ.....RHEGLKNYKKTISRSPGK 478

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002:**

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2083.5	81.6	454	23	ABAB76124
2	2083.5	81.6	462	23	ABAB76126
3	1789.5	70.1	341	9	AAAP3200
4	1751	68.6	468	12	AAAR13061
5	1727.5	67.7	469	14	AAAR40384
6	1711	67.0	477	15	AAAR47450
7	1669	65.4	447	10	AAAP3037
8	1596	62.5	476	22	AAAB49243
9	1565.5	61.3	446	17	AAAW05829
10	1554.5	60.9	581	22	AAAB81972

11	1515	59.4	464	16	AAAR76088
12	1502	58.9	445	16	AAAR76085
13	1497.5	58.7	464	23	AAU72801
14	1493.5	58.5	465	16	AAAB66758
15	1484	58.2	599	17	AAAR90837
16	1480.5	58.0	448	14	AAAR43673
17	1479.5	58.0	448	17	AAAR97376
18	1472	57.7	456	23	AAE18370
19	1472	57.7	464	19	AAAB83041
20	1472	57.7	464	21	AAAB14747
21	1472	57.7	464	21	AAAB90897
22	1472	57.7	464	23	ABAB74866
23	1472	57.7	464	23	ABAB74866
24	1471.5	57.7	473	22	AAAB36206
25	1470.5	57.6	448	17	AAAR98443
26	1459.5	57.2	477	22	AAU14288
27	1458	57.1	451	21	AAAY93734
28	1456.5	57.1	448	11	AAAR06476
29	1456.5	57.1	452	20	AAAY29458
30	1456.5	57.1	452	21	AAAB30322
31	1456.5	57.1	452	21	AAAY77766
32	1456	57.1	461	14	AAAR44494
33	1454.5	57.0	452	19	AAAB69316
34	1452.5	56.9	551	22	ABAB56471
35	1450.5	56.8	466	5	AAAP40032
36	1448.5	56.8	475	17	AAAR93353
37	1447	56.7	475	13	AAAR20057
38	1445	56.6	476	18	AAAW01822
39	1445	56.6	476	19	AAAB63765
40	1445	56.6	476	23	AAU11646
41	1440	56.4	451	22	AAE12715
42	1439.5	56.4	475	18	AAW11641
43	1439.5	56.4	519	23	AAU81993
44	1434.5	56.2	475	18	AAW11639
45	1433	56.2	470	13	AAAR22757

ALIGNMENTS

RESULT 1

ABAB76124

ID ABAB76124 standard: Protein; 454 AA.

AC ABAB76124;

DT 15-JUL-2002 (first.entry)

DE Recombinant 4G10 antibody heavy chain.

KW Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer; diagnosis.

OS Unidentified.

FH Key Location/Qualifiers

FT Misc-difference 5 /note= "encoded by CAR"

PN WO200218443-A2.

PD 07-MAR-2002.

PF 30-AUG-2001; 2001WO-US26926.

PR 01-SEP-2000; 2000US-0653755.

PA (UPST-) UPSTATE BIOTECHNOLOGY INC.

PI Esinger D, Stiles L, Lamarche A, Jelinek T;

DR WPI; 2002-393728/42.

DR N-PSDB; ABL56966.

Db	294	AQTQTHREDYINSTLRVSTLPQHQDMMSKEFKCKYNNKDLSPERTISKIGLVRAP	353
QY	378	QVYLPPPAEQLSRKDYSLTCLVVGFGPGDISVEMTNSGHTENYKDTAPVLDSGYSFI	437
Db	354	QWYLPPPAEQLSRKDYSLTCLVVGFGPGDISVEMTNSGHTENYKDTAPVLDSGYSFI	413
QY	438	YSLNLMKTSKWEKTDSPFCNVNRHEGLKNYYLKKYTI SRSPGK	478
Db	414	YSLNLMKTSKWEKTDSPFCNVNRHEGLKNYYLKKYTI SRSPGK	454

RESULT 3
AAP83200
ID AAP83200 standard; Protein; 341 AA.
XX AC AAP83200;
XX DT 06-MAR-1992 (first_entry)
XX DE
Sequence encoded by mouse lgs gamma 2b gene.

Immunoglobulin; class gamma; antibody; immune response; Fc receptor;
effector molecule; constant region; heavy chain; complement.

OS	Mouse.	
XX		
FFH	Key	Location/Qualifiers
Domain		1..97
FT		/label= CH1
FT	Region	98..119
FT		/label= hinge
FT	Domain	120..234
FT		/label= CH3
FT	Domain	235..341
FT		/label= CH3
FT	Misc-difference	122
FT		/note= "This residue is Leu in mutant FI235"

W08807089-A.

XX
PD 22-SEP-1988.

18-MAR-1988: 88WO-GB00211

01-DEC-1987: 87GR-0028042

PR 18-MAR-1987; 87GB-0006425.
PR 10-AUG-1987. 87GB-0018807

PR 18-MAR-1988; 88WO-GE00211.
PR 01-JAN-1988: 88CR-0025480

IX
A
(MEDI-) MEDICAL DES COMMISSA

IX	Winter CD	Duncan AD	Duncan AD
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WPT. 1988-285542/10

N-PSDB; AAN82456.

Modified IgG class antibody - having at least one aminoacid

function

Example; Fig 3; 42pp; English.

Modified antibodies (Abs) having an altered Fc region with al

following residues replaced: 234, 235, 236 and 237; 235 by GLN and 236 by LEU.

CC xx	residue 297 of the heavy chain has Sequence 341 AA;	been changed to Ala.
SQ	Query Match Best Local Similarity 70.1%; Score 1789.5; DB 9; Length 341; Matches 336; Conservative 0; Mismatches 0; Indels 5; Gaps 1;	
QY	143 AKTTPTSPVPLAPGCGDITGGSSVTLACLKVGYPESVTVTWNSSGSLSSSVHFPALLQSG 202	
Db	1 AKTTPTSPVPLAPGCGDITGGSSVTLACLKVGYPESVTVTWNSSGSLSSSVHFPALLQSG 60	
QY	203 LYTMSSSVTVPSSTWPSQTWCVSAHPASSTTVDDKLEPSSGPISTINPCPPCKECHKCPA 262	
Db	61 LYTMSSSVTVPSSTWPSQTWCVSAHPASSTTVDDKLEPSSGPISTINPCPPCKECHKCPA 120	
QY	263 PNLGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDV-----QLSWFVNNVEVHT 317	
Db	121 PNLGGPSVFIIPPNIKDVLMISLTPKVCVVVDVSEDDPDVDPGQLISWVFNVEVHT 180	
QY	318 AQOTQREDYNSTIRVVSTLPIQHODWMSGKEFKCVNNKNDLPSPERTISIKIGLVRA 377	
Db	181 AQOTQREDYNSTIRVVSTLPIQHODWMSGKEFKCVNNKNDLPSPERTISIKIGLVRA 240	
QY	378 QVYILPPPAQLSRKDVSLSLCLVGFNPGDISVWETNSGHTENKDTAPVLDSGVSFI 437	
Db	241 QVYILPPPAQLSRKDVSLSLCLVGFNPGDISVWETNSGHTENKDTAPVLDSGVSFI 300	
QY	438 YSKLNKMTSKWEKTSFSCNVRHEGLKNLYLKKTISRSPGK 478	
Db	301 YSKLNKMTSKWEKTSFSCNVRHEGLKNLYLKKTISRSPGK 341	

RESULT 4
AAR13061
ID AAR13061 standard; Protein; 468 AA.

XX
AC, AAR13061;XX
DT 03-OCT-1991 (first entry)XX
DE Monoclonal antibody OK3T heavy chain

XX OK3T; light chain: humanised antibody

XX
OS Mus musculus.

XX	Key	Location/Qualifiers
FH		

Peptide	1.19	/label= signal	nept
FT			
FT			

FT	Protein	20..468	/label= light chain
FT			

XX
PN
W09109967-A

XX
PD
11-JUL-1991

XX
PF 21-DEC-1990: 90WQ-CR02017

XX
PR 21-DEC-1990: 00H0-CB03017

PR 21-DEC-1989; 89GB-0028874.
XX

PA . (CELL-) CELLTECH LTD.

PPI Adair JR, Athwal DS, Emtage JS;

DR 1991-222915/30.
WPI;
N-DCDR: 1991-222915/30.
N-DCDR: 1991-222915/30.

XX
New Journal of Science

[illegible]

Db 370 VYVLPPEEMTKKQVTLTCMTDFMPEDIVVWNTNGKTELNYKNTPEVLDSGSGYFWY 429
 QY 439 SKLNKTSKWEKTDGSCNVRHEGLKNYLLKTTISRSPGK 478
 Db 430 SKLRVEKNWVERNSYSCSVVHEGLNHHTTSFSRTPGK 469

RESULT 6
 AAR47450
 ID AAR47450 standard; Protein; 477 AA.
 AC AAR47450;
 DT 24-JUN-1994 (first entry)
 XX T84.12 Heavy chain.
 XX Chimeric; Carcinoembryonic antigen; CCA; murine; mouse; constant;
 KW region; transmembrane; myeloma cell; light chain; tumour.
 XX Synthetic.
 XX W09325237-A.
 XX 23-DEC-1993.
 XX 15-JUN-1993; 93WO-0505709.
 XX 15-JUN-1992; 92US-0904074.
 XX (CITY) CITY OF HOPE.
 XX (YANG/) YANG Y.
 XX Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;
 Yang YH;
 WPI; 1994-007204/01.
 N-PSDB; AAQ54652.
 New chimeric T84.12 antibody active against carcinoembryonic
 antigen - has murine variable and human constant regions, also
 DNA encoding it and transformed myeloma cells
 Claim 1; Page 17; 27pp; English.
 The sequences (AAQ54651-52) show the light and heavy chain cDNAs
 of murine T84.12. The T84.12 antibody is directed against the
 tumour marker carcinoembryonic antigen, and is useful for
 tumour imaging and immunotherapy.
 The amino acid sequence given in the specification has been
 incorrectly identified as a nucleic acid sequence, therefore
 unacceptable characters have been represented as an 'N'.
 The amino acid sequence given below has been derived from the
 cDNA, by the indexer.

Q Sequence 477 AA;
 Query Match 67.0%; Score 1711; DB 15; Length 477;
 Best Local Similarity 69.1%; Pred. No. 2e-103;
 Matches 326; Conservative 53; Mismatches 83; Indels 10; Gaps 3;
 Y 7 LFLVTPFPCVLSQVQLKQSGPLQVPSQSLTCTVSGFSLTSYGVHWYRQSPGKLEW 66
 b 16 LIFLVLVGLVQVEKLVESGGGFGVPGGSLKLSCAASGFTSSYAMSVMYRQTPKRLW 75
 Y 67 LGVWISGGDTDYNAAFISRLSISKDNSKQLFPKMSLRATDTAIYYCARNRGDIYDFT 126
 b 76 VASISDGGITFFYVDSYKGRFTVSRDNARILYLQMSLSRSEDATMYCAR----IDYGG 131
 Y 127 YAMDYWGQCTSVTVSSAKTTPPSVYPLAPCGDGTGSSVTLGLVKGYPESVTVTWNSG 186
 b 132 GGFVWGQGTLATVSAKATAPSVYPLAPVCGDGTGSSVTLGLVKGYPPEVPTLWNSG 191

QY 187 SLSSSVHTPALLQSLGYLTMSSVTPSPSTWPSQTVCSTVAHPASSTVDKLEPSGPIS 246
 Db 192 SLSSGVHTPFAVLQSDLYTLSSSVTTPSTWPSQSTCNVAHPASSTKVDKKTIEPRCP-- 249
 QY 247 TINPCPPCKECHKCAPNLEGSPSVIFPPNIDVLMISLTPKVTVCVVVDVSEDDPDVQI 306
 Db 250 TIKPCPPC-----KCAPNLLGGSPSVIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQI 305
 QY 307 SWFVNNVEVHTAQTHREDYNSTIRVWSTLPIQHODWMSGKEFKCKVNNKDLPSPIERT 366
 Db 306 SWFVNNVEVHTAQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERT 365
 QY 367 ISKIKGLVRAPQVYILPPPAEQLSRSDVSLTCLVGFNPGDISVEMTSGHTEENYKDTA 426
 Db 366 ISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMTDFMPEDIVVWNTNGKTELNTKTE 425
 QY 427 PVLDSGSGYFIYKLMNMTSKWEKTDGSCNVRHEGLKNYLLKTTISRSPGK 478
 Db 426 PVLDSGSGYFMYSKLRVEKNWVERNSYSCSVVHEGLNHHTTSFSRTPGK 477

RESULT 7
 AAP93037
 ID AAP93037 standard; protein; 447 AA.
 XX AAP93037;
 AC AAP93037;
 DT 14-MAR-1990 (first entry)
 XX Chimeric antibody heavy chain variable region.
 XX Mus.
 XX KSL/4; chimeric antibody; heavy chain variable region;
 KW EP338767-A.
 XX 25-APR-1989.
 PD 18-APR-1989; 89EP-0303814.
 PF 21-APR-1988; 88US-0184522.
 PR (ELIL) ELI LILLY AND CO.
 PA Beavers LS, Bumol TF, Gadski RA, Weigel BJ;
 PI WPI; 1989-311203/43.
 DR N-PSDB; AAN91659.
 DR Recombinant DNA cpds. producing antibodies - monoclonal and
 PT chimeric derived from monoclonal antibody KSL/4.
 XX Claim 6; page 50; 89pp; English.
 XX The sequence encodes the heavy chain of MAb KSL/4, used to
 CC construct mouse/human chimeric antibodies. KSL/4 is a murine antibody
 CC which binds to surface antigens on adenocarcinoma cells and the use of
 CC human C regions avoids immunological problems during treatment.

SQ Sequence 447 AA;
 Query Match 65.4%; Score 1669; DB 10; Length 447;
 Best Local Similarity 68.5%; Pred. No. 1e-100;
 Matches 317; Conservative 52; Mismatches 74; Indels 20; Gaps 6;
 QY 20 QVOLKQSGGLVQPSQSLSTCTVSG--SLTSYGVHWYRQSPGKLEWLVWSG---GDT 76
 Db 1 QIQLVQSGPELKPGETVTKISCKASG--TETNYGMWYKQTPGKLGKWMG--WINTYTGEP 58
 QY 77 DYNAAFISRLSISKDNSKQLFPKMSLRATDT--AIYYCARNRGDIYDFTYAMDYWGQ 135
 Db 59 TYADDFGKGFASLETSASTAFLOIQ--PQNRTMAYTCVCR-----FISKGDYWGQ 110

136	TSVTSSAKTTTPSVYPLAPCGDGTGSSVTLGCLVGYFFESVTVTWNSGLSSVHTE	195	6	LLFCLVTPSPCVLSQVQLKSGQGLVQPSQSLSITCTVSGFSLTSGYVHWVQSPGKGL	65
111	TSVTSSAKTTAPSVYPLAPCGDGTGSSVTLGCLVGYFFEPVTLTWNSGLSSGVHTE	170	Db	6	ILFLVATATGVSXVQLKSGQGLVQPSQSLSITCTVSGFSLTSGYVHWVQSPGKGL
196	PALQSGLYTMSSSVTPSWPSTQVTCVAHPASSTTVVKKLPSGPISTINPCPPCK	255	QY	66	WLGVTWSGGDYNNAAFISRLSISKDNKSQSLFFKMNLSLRATDTAIYYCARNRGDIYDF
171	PAVLQSDLYTLSSSVTVTSWPSQITCNVAHPASSTKVKKIEPRGP--TIKPPPC-	227	Db	66	WLGVTWAGSTNYNSALMSRJSISKDNKSQSLFFKMNLSLRATDTAIYYCARNRGDIYDF
256	ECHKCPAPNLGGSPSVTFPPNPKDVLMSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEV	315	QY	126	T---YAMDYWGQTSVTVSSAKTTTPSVYPLAPCGDGTGSSVTLGCLVGYFFESVTV
228	---KCPAPNLGGSPSVTFPPNPKDVLMSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEV	284	Db	126	SVLTHSNFNGQTSVTVSSAKTTTPSVYPLAPCGDGTGSSVTLGCLVGYFFESVTV
316	HTAQOTQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDLPSPIERTISKIKGLVR	375	QY	182	TWNSGLSSSVHTEFPALQ--SGLYTMSSSVTPSWPSTQVTCVAHPASSTTVVKKL
285	HTAQOTQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDLPSPIERTISKIKGLVR	344	Db	186	SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKYE
376	APQVYILPPPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTEENYKDTAPVLDSGYS	435	QY	241	PSGPISTINPCPPCKECHKCAPNLGGSPSVTFPPNPKDVLMSLTPKVTCTVVDVSE
345	APQVYILPPPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTEENYKDTAPVLDSGYS	404	Db	246	PKSCDKT--HTCPP-----CPAPELLGGSPSVTFPPNPKDVLMSLTPKVTCTVVDVSE
436	FYSKLNKMTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK 478		QY	301	DPDVQISWFFVNNVEVHTAQOTQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDL
405	FYSKLNKMTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK 478		Db	299	DPEVFNWYVDGVEVHNNAKTPREQINSTYRVSVTLVHQLDNLGCKEYCKVSNKALP
			QY	361	SPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTE
			Db	359	APIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVGFNPGDISVEMTSNGHTE
			QY	421	NYKDTAPVLDSGYSFYSKLNKMTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK
			Db	419	NYKDTAPVLDSGYSFYSKLNKMTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK
RESULT 8					
AAB49243					
AAB49243					
15-MAR-2001 (first entry)					
Chimeric 4H6 anti-DR4 antibody heavy chain protein.					
Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis; autoimmune.					
Homo sapiens.					
Synthetic.					
WO200073349-A1.					
07-DEC-2000.					
25-MAY-2000; 2000WO-US14599.					
28-MAY-1999; 99US-0322875.					
(GETH) GENENTECH INC.					
Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;					
WPI; 2001-041145/05.					
Novel anti-death receptor 4 antibodies useful for treating cancer and immune related disorders such as rheumatoid arthritis, sjogren's syndrome, Grave's disease and diabetes mellitus					
Claim 16; Fig 18; 126pp; English.					
The present invention relates to an anti-Death receptor 4 (DR4) antibody. The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating an immune-related disease in a mammal such as arthritis and autoimmune disease.					
Sequence 476 AA;					
Query Match 62.5%; Score 1596; DB 22; Length 476;					
Best Local Similarity 63.8%; Pred. No. 6.le-96;					
Matches 305; Conservative 65; Mismatches 96; Indels 12; Gaps 4;					

SQ	Sequence	445 AA;
Query Match	58.9%; Score 1502; DB 16; Length 445;	
Best Local Similarity	61.3%; Pred. No. 7.4e-90;	
Matches	282; Conservative 68; Mismatches 94; Indels 16; Gaps 6;	
QY	20 QVQLKSGPLVQPSQSLTCTVSGFSTSYGVHWVWVROSPGKLEWLG-VIWSGGDTDY 78	
Db	1 QVQLQPGAEVLYKPGASVQLSKASGTYTGTGWIHWVWVROSPGKLEWLGVEVNPSTGRSDY 60	
QY	79 NAAFTSLRLSISKDNKSQLFFKMNLSLRATDIAIYCARNRDIYDFTYAMDYWGQTSV 138	
Db	61 NEKFNKATLTVDKSTTAYMQLSSTSDSAVYYCARERA---YGYDDAMDYWGQTSV 117	
QY	139 TVSSAKTPPSVYPLAPGCGDTGSSVTLGCLVKGVEPESVTVWNSGSLSSVHTFPAL 198	
Db	118 TVSSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGIFPEPVTWNSGSLSSVHTFPAL 177	
QY	199 LOSGLYTWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISINPCPPCKECH 258	
Db	178 LOSGLYTWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSPGISINPCPPCKECH 258	
QY	259 KCPAPNLEGGSGVFPPNIDKVLMSLTPKVCVVVDVSDDDPDVQISWVNNVEVHTA 318	
Db	229 ICTVPEVS---SVFIPPKPKDVLTLTPKVCVVVDVSDDDPDVQISWVNNVEVHTA 285	
QY	319 QTQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDLPLSPPIERTISKIGLVRAPQ 378	
Db	286 QTQPREOFNSTFSVSELPIMHQDNLGKFKCRVNSAAPPAPTEKTSIKGRPKAQ 345	
QY	379 VYILPPPAQLSKDKVSLTCLVGVNPGDISVEWTSNGHTENYKDTAPVLDSGSGYFI 438	
Db	346 VYITPPPKQKQKDKVSLTCLVGVNPGDISVEWTSNGHTENYKDTAPVLDSGSGYFI 405	
QY	439 SKLNKNTSKWEKTSFSCNVNREHGLKNTYLLKTTISRSPGK 478	
Db	406 SKLNKNTSKWEKTSFSCNVNREHGLKNTYLLKTTISRSPGK 445	
RESULT 13		
AAU72801	AAU72801 standard; protein; 464 AA.	
AAU72801;		
26-FEB-2002 (first entry)		
TRA-8 heavy chain.		
Tumour necrosis factor-related apoptosis-inducing ligand receptor;		
TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;		
autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;		
rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;		
Addison disease; scleroderma; Goodpasture's syndrome; sterility;		
myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;		
allergy; arteriosclerosis; myocarditis; cardiomyopathy;		
glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.		
Mus musculus.		
W0200183560-A1.		
08-NOV-2001.		
02-MAY-2001; 2001WO-US14151.		
02-MAY-2000; 2000US-201344P.		
(UABR-) UAB RES FOUND.		
Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;		
WPI; 2002-049338/06.		
N-PSDB; AAS97062.		
Novel antibody specific for tumour necrosis factor-related		
apoptosis-inducing ligand, useful for inhibiting cell proliferation in		
cancer -		
Claim 26; Page 198-199; 229pp; English.		
The invention describes a novel antibody which recognizes a tumour		
necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor		
DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing		
activity to a cell expressing DR5 in vivo. It is also useful for		
preparing a therapeutic for selective apoptosis of abnormal or		
dysregulated cells, and for inhibiting cell proliferation in a cell,		
preferably a human breast, ovary, colon, haematopoietic, prostate,		
lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may		
also be administered e.g. paclitaxel, taxol or cycloheximide. The		
antibody is used to treat an autoimmune disease, systemic lupus		
erythematosus, Hashimoto's disease, rheumatoid arthritis,		
graft-versus-host disease, Sjogren's syndrome, Chron's disease,		
pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,		
autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple		
sclerosis, Basedow's disease, insulin-dependent diabetes mellitus,		
allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,		
glomerular nephritis, hypoplastic anaemia, rejection after organ		
transplantation, and numerous malignancies of lung, prostate, liver,		
ovary, lymphatic or breast tissue. Peptides used to design primers for		
isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and		
AAU72802), TRA-8 are shown in AAU72799 and AAU72800.		
Sequence 464 AA;		
Query Match	58.7%; Score 1497.5; DB 23; Length 464;	
Best Local Similarity	61.1%; Pred. No. 1.5e-89;	
Matches	291; Conservative 66; Mismatches 100; Indels 19; Gaps 8;	
QY	4 LGLLCLVTFPPSVLQVQLKSGPLVQPSQSLTCTVSGFSTSYGVHWVWVROSPGK 63	
Db	5 LSLIF-LVLVLKGVQCEVLMVESGGGLVKPGSLKLSCAASGFTFSSVYVMSVWROTPEKR 63	
QY	64 LEWLVGVWSGGD-TDYNAAFISRLSISKDNKSQLFFKMNLSLRATDIAIYCARNRDIY 122	
Db	64 LEWLVGVWSGGD-TDYNAAFISRLSISKDNKSQLFFKMNLSLRATDIAIYCARNRDIY 119	
QY	123 YDFTYAMDYWGQTSVTVSSAKTPPSVYPLAPGCGDTGSSVTLGCLVKGVEPESVTV 182	
Db	120 -DSMITTDYWGQGTTLTVSSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGVEPESVTV 178	
QY	183 WNSGSLSSSVHTFPALQSLGTYWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSP 242	
Db	179 WNSGSLSSSVHTFPALQSLGTYWSSSVTVPSSTWPSQTVTCVAHPASSTVDKLEPSP 237	
QY	243 GPISTINPCPPCKEKCHKCPAPNLEGGSPVFTPPNIDKVLMSLTPKVCVVVDVSDDDP 302	
Db	238 -----RDC-GCKPC-ICTVPEVS---SVFIPPKPKDVLTLTPKVCVVVDVSDDDP 286	
QY	303 DVQTSWFVNNVEVHTAQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDLPLSP 362	
Db	287 EVQPSWEVDDVEVHTAQTHREDYNSTIRVSTLPIQHDWMSGKFKCKVNNKDLPLSP 346	
QY	363 IERTISKIGLVRAPQVYIPLPPPAQLSKDKVSLTCLVGVNPGDISVEWTSNGHTENY 422	
Db	347 IERTISKIGLVRAPQVYIPLPPPAQLSKDKVSLTCLVGVNPGDISVEWTSNGHTENY 406	
QY	423 KDTAPVLDSGSGYFIYSKLNKNTSKWEKTSFSCNVNREHGLKNTYLLKTTISRSPGK 478	
Db	407 KNTQPIIMDTGSGYFVYSKLNKNTSKWEKTSFSCNVNREHGLKNTYLLKTTISRSPGK 462	
RESULT 14		
AAU72801	AAU72801 standard; protein; 465 AA.	
AAU72801;		
26-FEB-2002 (first entry)		
TRA-8 heavy chain.		
Tumour necrosis factor-related apoptosis-inducing ligand receptor;		
TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;		
autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;		
rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;		
Addison disease; scleroderma; Goodpasture's syndrome; sterility;		
myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;		
allergy; arteriosclerosis; myocarditis; cardiomyopathy;		
glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.		
Mus musculus.		
W0200183560-A1.		
08-NOV-2001.		
02-MAY-2001; 2001WO-US14151.		
02-MAY-2000; 2000US-201344P.		
(UABR-) UAB RES FOUND.		
Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;		
WPI; 2002-049338/06.		

QY 249 NPCPPCKECHKCPAPNLEGGPSVIFPPNPKDVLMSLTPEKVTCTVVVDVSEDDPDVQISW 308
 Db 241 RDC-GCKPC-ICIVPEVS---SVFIPPPKPKDLTITLTPKVTCTVVVDISKDDPEVQFSW 295
 QY 309 FVNNVEVHTAQTOTHRDYNSTIRVSTLPIQHDQWMSGKEFKCKVNNKDLPSPIERTIS 368
 Db 296 FVDDVEVHTAQTOTPREQFNSTFRSVSELPIMHODWLNKGKFCRVNSAAPPAPPIEKTIS 355
 QY 369 KIKGLVRAPQVYIILPPPAEQLSRKDVSLTCLVVGCFNPGDISVENTSNGHTENYKDTAPV 428
 Db 356 KTRGRKAPQVYITIPPPEKQMAKDKVSLTCTMTDTFFEDITVEQWNGQPAENYKNTQPI 415
 QY 429 LDSGYSYFLYSKLNKMTSKWEKTDSCNVRHGLKNVYKTKTISRSPGK 478
 Db 416 MNTNGSYFVYSKLVQKNSWEAGNTFTCSVLHGLNHNHTEKLSLSHSPGK 465

RESULT 15

AAR90837
 ID AAR90837 standard; Protein: 599 AA.

AC AAR90837;

XX 25-JUN-1996 (first entry)

DE 3B1 single chain antibody from PCIB4631.

XX delta endotoxin; Bacillus thuringiensis; western corn rootworm;
 KW WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
 KW antibody.

OS Insecta sp.

XX W09600783-Al.

PN 11-JAN-1996.

PD 20-JUN-1995; 95WO-IB00497.

PF 28-JUN-1994; 94US-0267641.

XX (CIBA) CIBA GEIGY AG.

PI Carozzi NB, Koziel MG;

XX WPI: 1996-077494/08.

DR N-PSDB; AAT15733.

XX New monoclonal antibodies which bind insect gut proteins - used
 PT partic. with toxin moieties for the control of insect pests, partic.
 PT in plants

PS Claim 8; Page 68-72; 106pp; English.

XX AAR90829-39 are monoclonal antibodies or a binding fragments produced by
 CC using insect guts, partic. insect brush border membranes (BBMs), esp.
 CC corn rootworm, as antigen; immunising a donor animal with the antigen;
 CC isolating immunocompetent B cells from the immunised animal; fusing B
 CC cells with a tumour cell line; isolating the fused cells, culturing them
 CC and cloning positive hybrid cells; and screening the hybrid cells for
 CC prodn. of the required MABs. The MABs bind to the gut of a target insect
 CC but do not bind to mammalian BBMs. The DNA sequence can be operably
 CC linked to a toxin moiety, esp. selected from e.g. Bacillus toxins,
 CC Pseudomonas exotoxin and phytolaccin, etc.. The Abs are useful for
 CC control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
 CC Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
 CC maize.

XX Sequence 599 AA;

Query Match 58.2%; Score 1484; DB 17; Length 599;
 Best Local Similarity 60.5%; Pred. No. 1.5e-88;
 Matches 282; Conservative 70; Mismatches 90; Indels 24; Gaps 8;

AAR66758;

01-SEP-1995 (first entry)

Anti-tobacco mosaic virus monoclonal Ab heavy chain.

Tobacco mosaic virus; TMV; monoclonal antibody;
 heavy chain; virus-resistant plants; biofarming.

Synthetic.

Key Location/Qualifiers

Peptide 1..19

Peptide /label= leader

Peptide 20..465

Domain /label= mat_peptide

Domain 20..128

Domain /note= "variable heavy domain"

Domain 129..141

Domain /note= "J heavy 4 domain"

Domain 142..465

Domain /note= "constant heavy domain"

JP06319396-A.

22-NOV-1994.

07-MAY-1993; 93JP-0131208.

07-MAY-1993; 93JP-0131208.

(NTSB) JAPAN TOBACCO INC.

(KURS) KURARAY CO LTD.

WPI: 1995-040220/06.

N-PSDB; AAQ79930.

Transformed plant producing animal-derived anti-virus antibody -
 esp. tobacco plants producing anti-tobacco mosaic virus
 monoclonal antibody

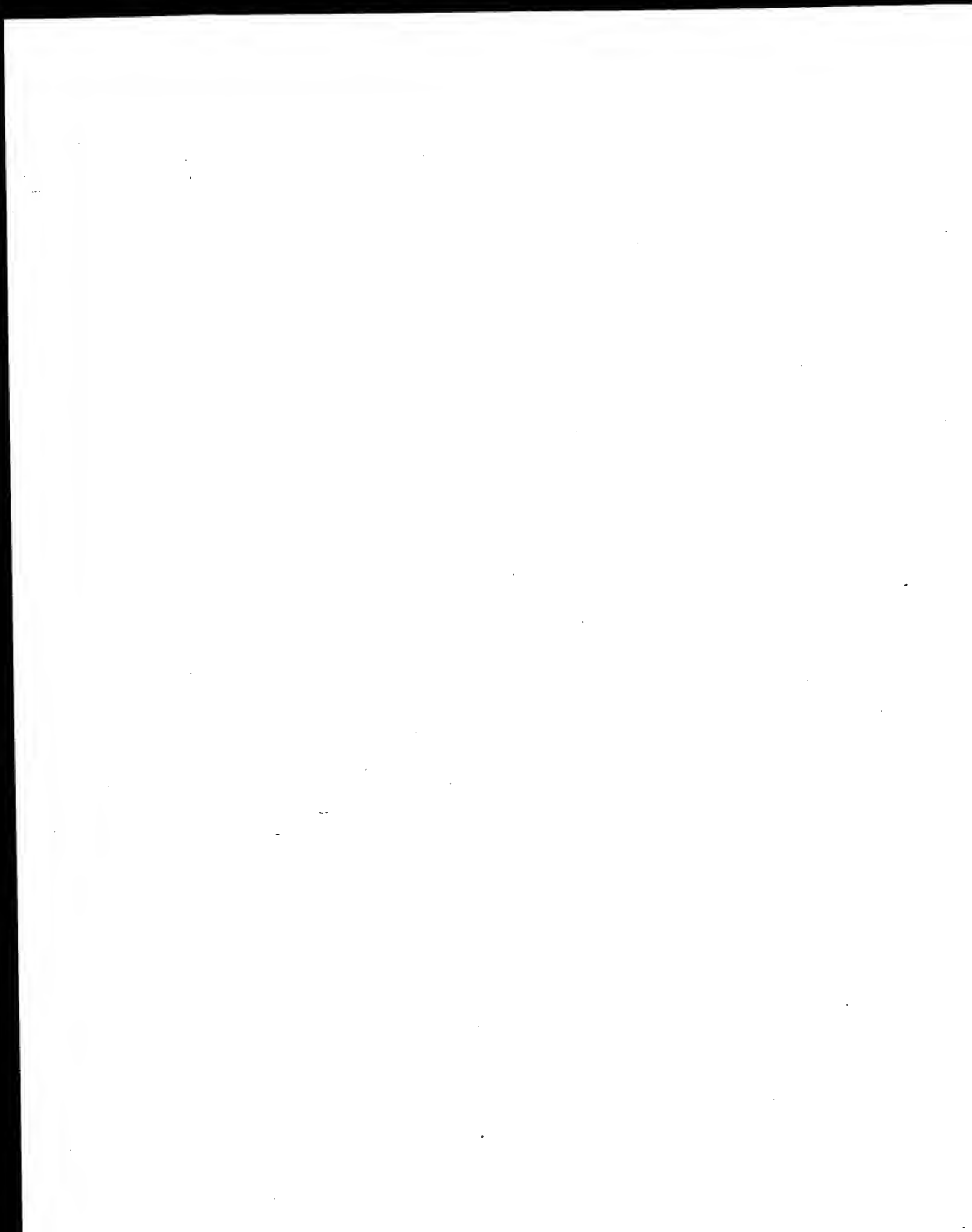
Example 2; Pages 14-15; 26pp; Japanese.

AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
 chains of an animal derived anti-tobacco mosaic virus (TMV)
 monoclonal antibody. The cDNAs were incorporated into a T1
 plasmid vector, which was incorporated into A. tumefaciens.
 The resultant plant expression vector was used to transform
 tobacco plants, making them TMV resistant, the plants could
 also be biofarmed for the prodn. of anti-virus antibodies.

Sequence 465 AA;

Query Match 58.5%; Score 1493.5; DB 16; Length 465;
 Best Local Similarity 60.0%; Pred. No. 2.8e-89;
 Matches 282; Conservative 73; Mismatches 100; Indels 15; Gaps 6;
 10 LVTFFSCVLSQLQKSGPLQPSQSLTCTVSGFSLTSYGVHVRQSPGKLEWLG 69
 10 ILSVTSGVSVQLQSQGAEALAPGASVLSCKASGYTFTSYMWQVQRPQGLEWIGA 69
 70 IWSG-GDITDYNAAFISRLSTSKDNKSQLEFFKMSLRATDTAIYICARNRGDIYDFTYA 128
 70 IYPGNGDTRYTKFKGKATLTADKSSSTAYMQLSALASEDSAVVYCAREGGYSWSD--YA 127
 129 MDYWGOGTSVTSSAKTTPPVYPLAPGCGDGTGSSVTLCGLVKGFPPSVVTVNWSGL 188
 128 MDYWGOGTSVTSSAKTTPPVYPLAPGSAQAQNTSMVTLGCLVKGFPEPVTVTVNWSGL 187
 189 SSSVHTFPALLQGLTYMTSSSVTVPSQVTCVAHPASSTTVDDKKLEPSPGISTI 248
 188 SSGVHTFPVQLQSDLYTLSSSVTVPSRPSSETVTCNVAHPASSTKVDDKIVP----- 240

Search completed: June 18, 2003, 16:44:18
Job time : 68.7921 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:08:07 ; Search time 1558.31 Seconds
(without alignments)
10174.698 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 acaccccttgcgtgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	878	89.7	939	11	AK002514 Mus muscu
2	702.8	71.8	896	13	BG969371 602836854
3	685.2	70.0	964	13	BG966302 602832780
4	674.4	68.9	935	11	BC031349 Mus muscu
5	674	68.8	805	13	BI454240 603170666
6	672.6	68.7	857	14	BQ960162 AGENCOURT

7	668.2	68.3	721	13	BG967689
8	640	65.4	871	14	BQ956722
9	637.2	65.1	944	12	BF687485
10	636.8	65.0	901	14	BQ943305
11	628	64.1	874	12	BG518527
12	620.8	63.4	950	12	BF162625
13	618.6	63.2	793	13	BI105963
14	607.6	62.1	712	13	BI100311
15	605	61.8	705	13	BG967208
16	594.4	60.7	967	12	BF687410
17	593.8	60.7	830	13	BI455041
18	592.4	60.5	974	14	BQ959869
19	590.4	60.3	823	12	BF580331
20	588.6	60.1	671	13	BM194931
21	586.6	59.9	778	13	BG964076
22	584.6	59.7	606	14	BQ922747
23	579	59.1	921	14	BQ924805
24	578.2	59.1	935	13	BG967882
25	577.2	59.0	764	13	BI455283
26	573.4	58.6	931	14	BQ959083
27	572	58.4	770	13	BG965872
28	571	58.3	611	14	BQ175762
29	571	58.3	781	13	BI152656
30	570.2	58.2	594	14	BQ175706
31	568	58.0	585	13	BM194777
32	567	57.9	886	14	BQ940987
33	566.6	57.9	915	14	BQ949447
34	566.2	57.8	785	14	BQ940341
35	561.8	57.4	959	14	BQ939046
36	558.2	57.0	607	12	BF580281
37	556.8	56.9	569	12	BF580308
38	554.2	56.6	643	12	BF579280
39	547.4	55.9	553	13	BM194877
40	547.2	55.9	926	14	BQ959057
41	545.4	55.7	674	12	BF582339
42	541.2	55.3	827	13	BI152061
43	540.6	55.2	698	13	BI109045
44	539.4	55.1	693	13	BM171763
45	536.4	54.8	851	13	BI101548

ALIGNMENTS

RESULT 1
AK002514
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

AK002514
Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010P20:immunoglobulin kappa chain variable 28 (V28), full insert sequence.
AK002514
GI:12832550
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
clone:0610010P20.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

939 bp mRNA linear HTC 19-JAN-2002

AK002514
Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010P20:immunoglobulin kappa chain variable 28 (V28), full insert sequence.

AK002514
GI:12832550

HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library

clone:0610010P20.

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

JOURNAL

MEDLINE

PUBMED

421 TGTGTCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAACTATCTGGAGGTGC 480
 493 CTCAGTCGTGTCTTCTTCAACAACTTCTACCCCAAGACATCAATGTCAAGTGGAGAT 552
 481 CTCAGTCGTGTCTTCTTCAACAACTTCTACCCCAAGACATCAATGTCAAGTGGAGAT 540
 553 TGATGGCAGTGAACGACAAAATGGCGTCTGAACTTGGAGCTTGAATGATCAGCAGCAGAA 612
 541 TGATGGCAGTGAACGACAAAATGGCGTCTGAACTTGGAGCTTGAATGATCAGCAGCAGAA 600
 613 CAGCAGCTTACAGATGAGCAGCAGCAGCAGTGTGACCAAGGAGGAGTATGAACGACATAA 672
 601 CAGCAGCTTACAGATGAGCAGCAGCAGTGTGACCAAGGAGGAGTATGAACGACATAA 660
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 781 CTATCTTCCCTTAAAGTCTTGGAGGCTTCCACCAAGGAGGAGTATGAACGACATAA 840
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 841 CTCGAAAGCTCTCCACCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
 913 TAATATTTGAGAAATATTTCAATAAAGTGAAGTCTTTTC 951
 901 TAATATTTGAGAAATATTTCAATAAAGTGAAGTCTTTTC 939

602836854F1 NCI_CGAP_Kid14 Mus musculus cdna clone IMAGE:4971397
 5', mRNA sequence.
 BG969371
 BG969371.1 GI:14357008
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 896)
 NIH-MGC <http://mgi.nhl.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cdna Library Preparation: Life Technologies, Inc.
 cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1A10956 row: k column: 14
 High quality sequence stop: 864.
 Location/Qualifiers
 1. 896
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4971397"
 /clone_lib="NCI_CGAP Kid14"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: kidney; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.75 kb. Constructed by Life

RESULT 2

IG969371

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT 238 a 237 c 201 g 220 t
 ORIGIN
 Query Match 71.88; Score 702.8; DB 13; Length 896;
 Best Local Similarity 90.88; Pred. No. 4.3e-99;
 Matches 815; Conservative 0; Mismatches 77; Indels 6; Gaps 6;
 QY 26 CACTGATCAGACAGTGCATGAGTGTGCTCAGTCAGTCTCCAGCCTCCCTATCTGATCT 85
 Db 1 CACTGATCAGACAGACATGAGTGTGCCACATCAGTGTGGGTGGTGTGCTGCTGCTGG 60
 QY 86 CTTACAGGTGCCAGATGTGACATCCAGATCAGTCTCCAGCCTCCCTATCTGATCT 145
 Db 61 CTTACAGATGCCAGATGTGACATCCAGATCAGTCTCCAGCCTCCCTATCTGATCT 120
 QY 146 GTGGGAGAACTGTCCACATCAGATGTCCAGCAAGTGGGAATATTCAAAATTTTAGCA 205
 Db 121 GTGGGAGAACTGTCCACATCAGATGTCCAGCAAGTGGGAATATTACAGTATTTAGCA 180
 QY 206 TGGTATCAGCAGACAGAGGAAAATCTCTCAGTCTCTGCTGCTGCTGCTGCTGCTGCT 265
 Db 181 TGGTATCAGCAGAAACAGGAAAATCTCTCAGTCTCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 266 GCAGATGGTGTGCCATCAAGTTCAGTGGCAGTGGATCAGGACACAAATATTCTCTCAAG 325
 Db 241 GGAGATGGTGTGCCATCAAGTTCAGTGGCAGTGGATCAGGACACAGTATTCCTCAAG 300
 QY 326 ATCAACAGCCTCAGCCTGAAGATTTTGGAGTATTACTGTCAACATTTTGGAGTACT 385
 Db 301 ATCAACAGCCTCAGTCTGAAGATTTTGGAGTATTACTGTCAACATTTTGGAGTACT 360
 QY 386 CGGTACAGTTCGGAGGGGGACCAAGCTGGAATAAAGGGCTGATGCTGCACCAACT 445
 Db 361 CGGTACAGTTCGGTGTGGGACCAAGTGGAGTCTGAAGGGCTGATGCTGCACCAACT 420
 QY 446 GTATCATCTTCCACATCAGTCCAGTGGAGTGAATTAACATCTGGAGTGGCTCAGTCTGTC 505
 Db 421 GTATCATCTTCCACATCAGTCCAGTGGAGTGAATTAACATCTGGAGTGGCTCAGTCTGTC 480
 QY 506 TTCTTGAACAACTTCTACCCCAAGACATCAATGTCAAGTGGAGATTTGATGGCAGTAA 565
 Db 481 TTCTTGAACAACTTCTACCCCAAGACATCAATGTCAAGTGGAGATTTGATGGCAGTAA 540
 QY 566 CGACAAATGGCTCCTGAACAGTTCAGTACAGGACAGCAAGACAGACCTACAGC 625
 Db 541 CGACAAATGGCTCCTGAACAGTTCAGTACAGGACAGCAAGACAGACCTACAGC 600
 QY 626 ATGAGCAGCAGCCTCAGCTTACCAAGGACGAGTATGAACGACA-TAACAGCTATACCTG 684
 Db 601 ATGAGCAGCAGCCTCAGCTTACCAAGGACGAGTATGAACGACA-TAACAGCTATACCTG 660
 QY 685 TGAGGCCACTCACAAGACATCACTTACCCATTGTCAAG-AGCTTCAACAGGAATGAGT 743
 Db 661 TGAGGCCACTCACAAGACATCACTTACCCATTGTCAAG-AGCTTCAACAGGAATGAGT 720
 QY 744 G-TTAGAGACAAAGTCTCT-CAGAGCCACACAGCTCCCGAGCTCCATCCTATCTTCC 801
 Db 721 GTTTAGAGACAAAGTCTCTGAGAGCGCCACACAGCTCCCGAGCTCCATCTCTATCTTCC 780
 QY 802 CTTCTAAGTCTTGGAGGCTTCCCAAGGACCTACCAAGTGTGGGCTGCTCCAAACC 861
 Db 781 CTTCTAAGTCTTGGAGGCTTCCCAAGGACCTACCAAGGACCTAAGCTGTGGGCTGCTCCAA 838
 QY 862 TCCTCCCAAGCT 919
 Db 839 TCCTCCCAAGCT

RESULT 3

BG966302

LOCUS

DEFINITION

602832780F1 NCI_CGAP_Co24 Mus musculus cdna clone IMAGE:4987626 5',

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: no cloning site / microdeletion.

FEATURES	source	microdeletion	location/Qualifiers
BASE COUNT	251 a	247 c	208 g
ORIGIN			
			1. .935
			/organism="Mus muscu
			/db_xref="taxon:1009
			/clone="IMAGE:15143
			/tissue_type="Mamma
			/clone_lib="Soares_L
			/lab_host="DH10B"
			/note="vector: pT7T

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BASE COUNT      251 a  247 c  208 g  229 t
ORIGIN
/note="Vector: pT/T3D-pac"

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Query Match	68.9%;	Score 674.4;	DB 11;	Length 935;
Best Local Similarity	84.3%;	Pred. No. 9,8e-95;		
Matches	789;	Conservative 0;	Mismatches 131;	Indels 16; Gaps 2;
57	CTCAGGTCCTGGCGTTCGTCTGCTGTGTGCTGTACAGGTGCCAGATGTGACATCCAGATGA	116		
1	CTGAGTTCCTGGGGCTGCTGTGCTCTGGATCCCTGGAGCCATTTGGGATATTGTGATGA	60		
117	CTCAGTCTCCAGCTCCCTATCTGCATCTGTGGGAGAAACATGTCCACATCATGTGCGAG	176		
61	CTCAGGCTGCACCTCTGTGACCTGTCACTCTCTGGAGAGTCAGTATTCATCTCTCTGCAGGT	120		
177	CAAAGTGGGAATATTC-----AAAATATTAGCATGGTATCAGCAGACAC	221		
121	CTAGTAAAGTCTCCTGCATATTGATGGCAACACTTATTATTTGGTTCCTGCGAGAGC	180		
222	AGGGAATAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCGAT	281		
181	CAGGCCAGTCTCCTCAGCTCCTGATATATCGGATGTCCAACTTTGCTCAGGAGTCCCGAG	240		
282	CAAAGTTTCAGTGGCAGTGGATCAGGAACACAAATATTCTCTCAAGATCAACAGCGCTGCAGC	341		
241	ACAGGTTTCAGTGGCAGTGGGTCAGGAACCTGCTTTACACTGAGAACTCAGTAGAGTGGAGG	300		
342	CTCAAGATTTTGGGAGTTATTACTCTCAACATTTTGGAGTACTCCGTACACGTTTCGGAG	401		
301	CTGAGGATGTGGTGTATTACTGTATGTCACACATCTAGAAATATCCGTACACGTTTCGGAG	360		
402	GGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCAC	461		
361	GGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCAC	420		
462	CATCAGTTCAGGAGTTACATCTCGAGGTGGCTCAGTCGTGTGCTTCTTGAACAACTTCT	521		
421	CATCAGTTCAGGAGTTACATCTCGAGGTGGCTCAGTCGTGTGCTTCTTGAACAACTTCT	480		
522	ACCCCAAGAGCATCAATCTCAAGTGGAGATTGATGGCAGTGAACGACAAATATGGCGTCC	581		
481	ACCCCAAGAGCATCAATCTCAAGTGGAGATTGATGGCAGTGAACGACAAATATGGCGTCC	540		
582	TGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCACTTACAGCATGAGCAGCACCTCA	641		
541	TGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCACTTACAGCATGAGCAGCACCTCA	600		
642	GTTGACCAAGGACGATGTAACGACATCAACAGCTATACCTGTGAGGGCACTTCAACAGA	701		
601	CGTTGACCAAGGACGATGTAACGACATCAACAGCTATACCTGTGAGGGCACTTCAACAGA	660		
702	CATCAACTTCACCATTTGTCAAGAGCTTCAACAGGAATGAGTGTTAGACACAAAGTCTCT	761		
661	CATCAACTTCACCATTTGTCAAGAGCTTCAACAGGAATGAGTGTTAGACACAAAGTCTCT	720		
762	GAGACGCCACACCCAGCTCCCGAGTCCATCTCTTCTCCCTTCTTAAGGCTTTGAGGCT	821		
721	GAGACGCCACACCCAGCTCCCGAGTCCATCTCTTCTCCCTTCTTAAGGCTTTGAGGCT	780		

Qy	822	TCCCCACAAGCAGCTACCACTGTTGC	GGTGTCCAAACCCTCTCCCACCTCTTC	C 881
Dδ	781	TCCCCACAAGGACCTACCACTGTTGC	GGTGTCCAACCTCTCTCCCACCTCTTC	C 840
Qy	882	TCCTCTCCCTTTCCCTGGCTTTATCAT	GCTAATAATTGCAGAAAAATTC	CAATAAGT 941
Dδ	841	TCCTCTCCCTCTTC - TGGCTTTATCAT	GCTAATAATTGCAGAAAAATTC	CAATAAGT 899
Qy	942	GAGTCTTTGCCAAAATAAAAAAAAAA	AAAAAAAAAAAAAAAAA	977
Dδ	900	GAGTCTTTGCATCTGAATAAAAAAAAA	AAAAAAAAAAAAAAAAA	935

RESULT 5
BI454240

LOCUS	BI454240	805 bp	mRNA	linear	EST 21-AUG-2001
DEFINITION	603170666F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5250017 5',				
ACCESSION	BI454240				
VERSION	BI454240				
KEYWORDS	EST.				
ORGANISM	house mouse.				
SOURCE	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 805)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-r@mail.nih.gov				
	Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LLAM11631 row: d column: 18				
	High quality sequence stop: 790.				

FEATURES	SOURCE
1. <i>General</i>	
2. <i>Specific</i>	
3. <i>Other</i>	
4. <i>Other</i>	
5. <i>Other</i>	
6. <i>Other</i>	
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97. <i>Other</i>	
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100. <i>Other</i>	

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BASE COUNT			
ORIGIN			180 t

Query Match	58.8%;	Score 674;	DB 13;	Length 805;
Best Local Similarity	94.0%;	Pred. No. 1.2e-94;		
Matches 756;	Conservative 0;	Mismatches 40;	Indels 8;	Gaps 5;

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[illegible]

[illegible]

RESULT 9	BF687485	944 bp	linear	EST 22-DEC-2000
ACCESSION	603102475F1	NCI_CGAP_Kid14	Mus musculus	cDNA clone IMAGE:4220563
DEFINITION	5', mRNA sequence.			
VERSION	BF687485			
KEYWORDS	BF687485.1	GI:11972893		
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Makayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 944)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: raaob@remail.nih.gov			

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov> row: f column: 20
Plate: LLAM9804
High quality sequence stop: 751.
Location/Qualifiers
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/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Kid14"
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/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Constructed by Life Technologies, Inc. This is a NCI CGAP library."

BASE COUNT	285 a	238 c	202 g	219 t		
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Best Local Similarity	90.9%;	pred. No. 5.1e-8;				
Matches 747;	Conservative 0;	Mismatches 63;	Indels 12;	Gaps 6;		
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DB	1	GTCA	CCATCATCATGTCGAGCAAGTGGGAATATTCACGATATTATTAACTGTATCAGCAG	60		
QY	218	ACACAGGGA	AAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGGTGTG	277		
DB	61	AAACAGGGA	AAATCTCCTCAGCTCCTGGTCTATAATGCAAAACCTTAGCAGATGGGTGTG	120		
QY	278	CCATCAAGGTT	CAGTGGCAGTGGATCAGGAACACAATATTTCTCAAGATCAACAGCCTG	337		
DB	121	TC	CCCAAGGTTTCAGTGGCAGTGGATCAGGAACAGATATTTCTCCAGATCCACAGTTTG	180		
QY	338	CAGCCTGAAGAT	TTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCGGTACACGTTC	397		
DB	181	CAGTTTGA	AGATTTGGGACTTATTACTGTCAACATTTTTGGAACTACTCCGTACACATTC	240		
QY	398	GGAGGGGG	CCACAGCTGGAAATAAACGGGCTGATGCTGCACCAACCTGTATCCCATCTTC	457		
DB	241	GGAGGGGG	CCACAGCTGGAAATAAACGGGCTGATGCTGCACCAACCTGTATCCCATCTTC	300		
QY	458	CCACCATC	AGTGCAGCACTTAACATCTCGAGTGCTCAGTCTGTGCTTCTTGGAACAC	517		
DB	301	CCACCATC	AGTGCAGCACTTAACATCTCGAGTGCTCAGTCTGTGCTTCTTGGAACAC	360		
QY	518	TTCTACCC	CAAGAGCATCAATGTC	CAAGTGGAGATTGATGGCAGTGAACAGCAAAATGGC	577	
DB	361	TTCTACCC	CAAGAGCATCAATGTC	CAAGTGGAGATTGATGGCAGTGAACAGCAAAATGGC	420	
QY	578	GTCCTGA	ACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCAC	637		
DB	421	GTCCTGA	ACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCAC	480		
QY	638	CTCAGCTG	TACCAAGACAGAGTATACACACATACACGTATACCTGTGAGGCCACTCAC	697		
DB	481	CTCAGCTG	TACCAAGACAGAGTATACACACATACACGTATACCTGTGAGGCCACTCAC	540		
QY	698	AGACATCA	ACTTACCCCATTCGAAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGG	757		
DB	541	AGACATCA	ACTTACCCCATTCGAAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGG	600		
QY	758	TCCTGAG	CGGCCACACACAGCTCCCGAGCTCCATCCTATCTTCCCTTCTAAGGCTTTGGA	817		
DB	601	T-CTGAG	AGCCACACACAGCTCCCGAGCTCCATCCTATCTTCCCTTCTAAGGCTTTGGA	658		
QY	818	GGCTTCCC	CCACAGCGACCTACACATGTTGGGTGTC	CTCAAACTCTCTCCCACTCCTT	877	

[illegible]

[illegible]

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577 CGTCTGAACAGTGGATCAGTGGATCAGAACACAATATCTCTCAAGATCAACAGCCT 636
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637 CTTTACCCCAAGACATCAATGTCAGTGGATCAGAACACAATATCTCTCAAGATCAACAGCCT 696
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599 CTTTACCCCAAGACATCAATGTCAGTGGATCAGAACACAATATCTCTCAAGATCAACAGCCT 657
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697 CAAGACATCAACTTCACCCATTCAGTGGATCAGAACACAATATCTCTCAAGATCAACAGCCT 756
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658 CAAGACATCAACTTCACCCATTCAGTGGATCAGAACACAATATCTCTCAAGATCAACAGCCT 717
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RESULT 13
LOCUS BI105963
DEFINITION 793 bp mRNA linear EST 26-JUN-2001
mRNA sequence.
BI105963
BI105963.1 GI:14556856

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 793)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1100 row: a column: 05
High quality sequence stop: 769.

Location/Qualifiers
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/clone="IMAGE:5036044"
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/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site:1; Salt;
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator

FEATURES
source

BASE COUNT 212 a 230 c 185 t
ORIGIN
Query Match 63.2%; Score 618.6; DB 13; Length 793;
Best Local Similarity 87.8%; Pred. No. 4e-86;
Matches 686; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

QY 188 ATTCAAAATTTATTTAGCATGGTATCAGCAGACACAGGGAATCTCCTCAGCTCTCGTGC 247
Db 10 AGTGAAATTTTCATCAGCTGGTATCAGCAGACAGGATCTCTCCCAAGCCCTGGATT 69
QY 248 TATTCGCAAAAACCTTAGCAGATGGTGCATCAAGTTTCAGTGGCAGTGATCAGGA 307
Db 70 TATCGTATATCGGACCTGGCTTCCTGAGTCCCTGCTCCTCAGTGGCAGTGGGACTGG 129
QY 308 ACACAATATTTCTCAAGATCAACAGCCTGAGCCTGAAGATTTTGGGAGTTATTACTGT 367
Db 130 ACCTCTTACTCTCAACAATCAGCAGCATGAGGCTGAAGATGCTGCCACTTATTTCCTGC 189
QY 368 CAACATTTTGGAGTACTCCGTACACGCTTCGAGGGGGGACCAAGCTGGAATAAAGCG 427
Db 190 CAGCAGTATCATAGTTTACCCACGGACCTTCGGTGGAGCCACCAAGCTGGAATCAAGCG 249
QY 428 GCTGATGCTGCACCAACTGTATCCATCTTCCCAACATCCAGTGAGCAGTTAACTCTGGA 487
Db 250 GCTGATGCTGCACCAACTGTATCCATCTTCCCAACATCCAGTGAGCAGTTAACTCTGGA 309
QY 488 GGTGCTCAGTCGCTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGG 547
Db 310 GGTGCTCAGTCGCTGCTTCTTGAACAACCTTACCCCAAGACATCAATGTCAAGTGG 369
QY 548 AAGATTGATGGCAGTGAACGACAAAATGGCTCCTGAAACAGTTGGACTGATCAGCAGACG 607
Db 370 AAGATTGATGGCAGTGAACGACAAAATGGCTCCTGAAACAGTTGGACTGATCAGCAGACG 429
QY 608 AAGACAGCCTTACAGCATGAGCAGCACCCCTCAGTTGACCAAGGAGCAGTATGAACGA 667
Db 430 AAGACAGCCTTACAGCATGAGCAGCACCCCTCAGTTGACCAAGGAGCAGTATGAACGA 489
QY 668 CATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTTGCAAGACG 727
Db 490 CATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTTGCAAGACG 549
QY 728 TTCAACAGGAATGAGTGTAGAGACAAAGCTCTGAGACGCCACCCAGCTCCCCAGCT 787
Db 550 TTCAACAGGAATGAGTGTAGAGACAAAGCTCTGAGATGCCACCCAGCTCCCCAGCT 609
QY 788 CCATCCTATCTTCCCTTCTAAGGCTTTGGAGGCTTCCCAACAGCGACCTACCACTGTTG 847
Db 610 CCATCCTATCTTCCCTTCTAAGGCTTTGGAGGCTTCCCAACAGCGACCTACCACTGTTG 669
QY 848 CGTGTCTCAAACTCCTCCTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 907
Db 670 CGTGTCTCAAACTCCTCCTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 729
QY 908 CATGCTAAATTTGAGAGAAATATTCAA-TAAAGTGAGTCTTTGCAAAAAAATAAAAAA 966
Db 730 CATGCTAAATTTGAGAGAAATATTCAA-TAAAGTGAGTCTTTGCAAAAAAATAAAAAA 789
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Db 790 A 790

RESULT 14
LOCUS BI100311
DEFINITION 712 bp mRNA linear EST 26-JUN-2001
5', mRNA sequence.
ACCESSION BI100311
VERSION BI100311.1 GI:14551204
KEYWORDS EST.

Page 12

24	CCACAAGCGACCTACCACTGTTGGGGTCTCCAAACCTCTCCGCCACCTCTCTCTCCCTC	883
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60	CTCTCTCCCTTCCCTTGGCTTTATCATGCTATATTTGCAGAAAAATATTCAATAAAGTGA	664
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BG967208		
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SOURCE	house mouse	
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REFERENCE	1 (bases 1 to 705)	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs@email.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	

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FEATURES
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                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.6 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT   199 a    196 c    148 g    162 t
ORIGIN
Query Match          61.8%; Score 605; DB 13; Length 705;
Best Local Similarity 91.4%; Pred No. 5,3e-84;
Matches 641; Conservative 0; Mismatches 60; Indels 0; Gaps 0
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Dd      1 CAGACAGGTTTCAGTGGCAGTGATCAGGCAGAGATTTTCACACTCCAAGATTCAGCAGAGTGG 60
QY      339 AGCCTGAAGATTTGGGAGTTATTACTCTCAACATTTTGGAGTAGTCTCGGTACACAGTTCGG 398
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      61 AGGCTGAGGATCTGGGAGTTTATTCTCTCAAGTACACATGTTCCATTCACGTTCC 120
QY      399 GAGGGGGACCAAGCTGGAAATAAACCAGGCTGATGCTGCACCACTGTATCCATCTTCCC 458
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd      121 GCTCGGGACAAAGTTGGAAATAAACACGGCTGATGCTGCACCAACTGTATCCATCTTCCC 180
QY      459 CACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTTGCTTCTTTGAACAACAT 518

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181 CACCATCCAGTGGAGGTTAAACATCTGGAGTGCCCTCAGTCTGGTGCTCTTGGAACT 240
519 TCTACCCCAAGACATCAATGTCAGTGAAGATTCATGGCAGTGAACGACAAAATGGCG 578
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579 TCTGAAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCC 538
301 TCTGAAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCC 360
639 TCACCTTGACCAAGGACGAGTATGAACGACATACAGGCTATACCTGTGAGGCCACTCACA 698
361 TCACCTTGACCAAGGACGAGTATGAACGACATACAGGCTATACCTGTGAGGCCACTCACA 420
699 AGACATCAACTTCACCCATTGTCAGAGGCTTCAACAGGAATGAGTGTAGAGACAAAGGT 758
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759 CCTGAGAGCCACACAGCTCCCGAGCTCCATCTCTTCCCTTCTAAGGTCTTGGAG 818
481 CCTGAGAGCCACACAGCTCCCGAGCTCCATCTCTTCCCTTCTAAGGTCTTGGAG 540
819 GCTTCCCAAGGACGACCTACACTGTTGGGCTGCTCCAAACCTCCTCCGACCTCTTC 878
541 GCTTCCCAAGGACGACCTACACTGTTGGGCTGCTCCAAACCTCCTCCGACCTCTTC 600
879 TCCTCCCTCCCTTCTTCTTGGCTTTTATCATGCTAATTTGAGAAAATATTCAATAA 938
601 TCCTCCCTCCCTTCTTCTTGGCTTTTATCATGCTAATTTGAGAAAATATTCAATAA 660
939 AGTGAAGTCTTTGCAAAAAAATAAAAAAATAAAAAA 979
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Search completed: June 24, 2003, 01:20:04
Job time : 1567.31 secs

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3	3	733.6	74.9	998	10	US-10-219-051B-I4373	Sequence 3	
4	4	576.6	58.9	2221	9	US-10-144-771-21147	Sequence 4	
5	5	524.6	53.6	959	10	US-10-219-051B-12710	Sequence 5	
6	6	482.6	49.3	633	9	US-10-236-051-7	Sequence 6	
7	7	471.4	48.2	870	10	US-10-424-599-65669	Sequence 7	
8	8	461.4	47.1	705	1	PTCT-US02-34420A-22	Sequence 8	
9	9	461.4	47.1	705	1	PTCT-US02-35333A-22	Sequence 9	
10	10	461.4	47.1	705	9	US-10-286-132A-22	Sequence 10	
11	11	461.4	47.1	705	9	US-10-281-479A-22	Sequence 11	
12	12	461.4	47.1	705	10	US-10-275-180A-22	Sequence 12	
13	13	447.8	45.7	1526	6	US-09-726-219A-189	Sequence 13	
14	14	446.6	45.6	714	10	US-10-384-933-10	Sequence 14	
15	15	445.2	45.5	702	8	US-10-251-215-47	Sequence 15	
16	16	440.6	45.0	990	8	US-10-458-714-79	Sequence 16	
17	17	426.2	43.5	943	1	PTCT-US03-01096-125	Sequence 17	
18	18	422.2	43.1	645	9	US-10-236-051-3	Sequence 18	
19	19	420.2	42.9	941	8	US-10-458-714-81	Sequence 19	
20	20	420.2	42.9	941	10	US-10-450-027-183	Sequence 20	

Downloaded from <http://ajph.org/> on November 10, 2014

Count	No.	Score	Query	Match	Length	DB	ID	Description
1	1	733.6	74.9	998	10	US-10-219-051B-3410	Sequence 1	
2	2	733.6	74.9	998	10	US-10-219-051B-12785	Sequence 2	
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4	4	576.6	58.9	2221	9	US-10-144-771-21147	Sequence 4	
5	5	524.6	53.6	959	10	US-10-219-051B-12710	Sequence 5	
6	6	482.6	49.3	633	9	US-10-236-051-7	Sequence 6	
7	7	471.4	48.2	870	10	US-10-424-599-65669	Sequence 7	
8	8	461.4	47.1	705	1	PTCT-US02-34420A-22	Sequence 8	
9	9	461.4	47.1	705	1	PTCT-US02-35333A-22	Sequence 9	
10	10	461.4	47.1	705	9	US-10-286-132A-22	Sequence 10	
11	11	461.4	47.1	705	9	US-10-281-479A-22	Sequence 11	
12	12	461.4	47.1	705	10	US-10-275-180A-22	Sequence 12	
13	13	447.8	45.7	1526	6	US-09-726-219A-189	Sequence 13	
14	14	446.6	45.6	714	10	US-10-384-933-10	Sequence 14	
15	15	445.2	45.5	702	8	US-10-251-215-47	Sequence 15	
16	16	440.6	45.0	990	8	US-10-458-714-79	Sequence 16	
17	17	426.2	43.5	943	1	PTCT-US03-01096-125	Sequence 17	
18	18	422.2	43.1	645	9	US-10-236-051-3	Sequence 18	
19	19	420.2	42.9	941	8	US-10-458-714-81	Sequence 19	
20	20	420.2	42.9	941	10	US-10-450-027-183	Sequence 20	

[illegible]

RESULT 6
US-10-236-051-7
: Sequence 7, Application US/10236051
: GENERAL INFORMATION:
: APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
: APPLICANT: LETURCO, Didier J.
: APPLICANT: MORIARTY, Ann M.
: APPLICANT: ULEVITCH, Richard J.

418 AATAAAACGGGCTGATGCTGCACCAAACTGTATCCATCTTCCACCATCCAGTGGACGATT 477
|||||
1664 AATAAAACGGGCTGATGCTGCACCAAACTGTATCCATCTTCCACCATCCAGTGGACGATT 1723
|||||
478 AACATCTGGAGGTGCCTCAGTCTGTGTCTTCTTGAACAACCTCTACCCCAAGACATCAA 537
|||||
1724 AACATCTGGAGGTGCCTCAGTCTGTGTCTTCTTGAACAACCTCTACCCCAAGACATCAA 1783
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538 TGTCAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCTTGAACAGTTGACTGA 597
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1784 TGTCAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCTTGAACAGTTGACTGA 1843
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598 TCAGGACAGCAAAAGACAGCAGCTACAGCATGAGCAGCACCCTCAGCTTGAACAAGGACGA 657
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1844 TCAGGACAGCAAAAGACAGCAGCTACAGCATGAGCAGCACCCTCAGCTTGAACAAGGACGA 1903
|||||
658 GTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCAT 717
|||||
1904 GTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCAT 1963
|||||
718 TGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGGTCCTGAGAGCCGACCAACGAG 777
|||||
1964 TGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAGGTCCTGAGAGCCGACCAACGAG 2023
|||||
778 CTCGCCAGCTCATCTATCTTCCCTTCTTAAGTCTTGGAGGCTTCCGCCACAAAGCGACCT 837
|||||
2024 CTCGCCAGCTCATCTATCTTCCCTTCTTAAGTCTTGGAGGCTTCCGCCACAAAGCGACCT 2083
|||||
838 ACCACTGTTGCGGTGCTCCAAACCTCCTCCCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
|||||
2084 ACCACTGTTGCGGTGCTCCAAACCTCCTCCCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2143
|||||
898 TGGCTTTTATCATGCTAATATTGTCAGAAAAATATCAATAAAGTGAGTCTTTGCCAAAAA 957
|||||
2144 TGGCTTTTATCATGCTAATATTGTCAGAAAAATATCAATAAAGTGAGTCTTTGCACCTGA 2203
|||||
958 AAAAAAIAAAAAAAAAA 974
|||||
2204 GATACAAGACACACACA 2220
|||||

RESULT 5
3-10-219-051B-12710
Sequence 12710, Application US/10219051B
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219, 051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12710
LENGTH: 959
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: EMBL / L22655
DATABASE ENTRY DATE: 2000-03-04
3-10-219-051B-12710

Query Match	53.68	Score 524.6	DB 10	Length 959
Best Local Similarity	75.38	Pred. No. 5e-90		
Matches 716: Conservative	0	Mismatches 209	Indels 26	Gaps 4

RESULT 5
 3-10-219-051B-12710
 Sequence 12710, Application US/10219051B
 GENERAL INFORMATION:
 APPLICANT: The General Hospital Corporation doing business as Massachusetts General
 APPLICANT: Hospital / Bayer AG
 TITLE OF INVENTION: Nucleotide sequences involved in pain
 FILE REFERENCE: Lea 35693 Foreign Countries
 CURRENT APPLICATION NUMBER: US/10/219, 051B
 CURRENT FILING DATE: 2003-05-09
 PRIOR APPLICATION NUMBER: US 60/312,147
 PRIOR FILING DATE: 2001-08-14
 PRIOR APPLICATION NUMBER: US 60/346,382
 PRIOR FILING DATE: 2001-11-01
 PRIOR APPLICATION NUMBER: US 60/333,347
 PRIOR FILING DATE: 2001-11-26
 NUMBER OF SEQ ID NOS: 14715
 SOFTWARE: Perl script
 SEQ ID NO 12710
 LENGTH: 959
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: EMBL / L22655
 DATABASE ENTRY DATE: 2000-03-04
 3-10-219-051B-12710

; APPLICANT: TOBIAS, Peter S.
 ; APPLICANT: MATHISON, John C.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
 ; FILE REFERENCE: SCRIPT1140-4
 ; CURRENT APPLICATION NUMBER: US/10/236,051
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 09/170,769
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: US 08/373,297
 ; PRIOR FILING DATE: 1995-01-23
 ; PRIOR APPLICATION NUMBER: PCT/US94/05898
 ; PRIOR FILING DATE: 1994-05-27
 ; PRIOR APPLICATION NUMBER: US 08/070,160
 ; PRIOR FILING DATE: 1993-05-28
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 633
 ; TYPE: DNA
 ; ORGANISM: Murine
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(633)
 ; OTHER INFORMATION: CDR1=Nucleic acids 61-93; CDR2=Nucleic acids 139-159;
 ; OTHER INFORMATION: CDR3=Nucleic acids 256-28
 ; 10-10-236-051-7

Query Match		49.3%;	Score 482.6;	DB 9;	Length 633;
Best Local Similarity		85.2%;	Pred. No. 4.5e-82;		
Matches 539;		Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;
113	ATGACTCAGTCTCCAGCCTCCCTATCTGTCATCTGTGGGAAACTGTCCACATACATGT	172			
114		173			
115		174			
116		175			
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122		181			
123		182			
124		183			
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211		270			
212		271			
213					

Db	601	CCCATGTGTCAGAGCTTCACAGGAATGAGTGT	633
RESULT 7			
US-10-424-599-65669			
; Sequence 65669, Application US/10424599			
; GENERAL INFORMATION:			
; APPLICANT: La Rosa Thomas J			
; APPLICANT: Kovalic David K			
; APPLICANT: Zhou Yihua			
; APPLICANT: Cao Yongwei			
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and			
; TITLE OF INVENTION: Plants and Uses Thereof for			
; FILE REFERENCE: 38-21(53223)B			
; CURRENT APPLICATION NUMBER: US/10/424,599			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 285684			
; SEQ ID NO 65669			
; LENGTH: 870			
; TYPE: DNA			
; ORGANISM: Glycine max			
; FEATURE:			
; OTHER INFORMATION: Clone ID: PAT_MPT3847_30314C			
US-10-424-599-65669			

Query Match	48.2%	Score	471.4	DB	10	Length	870
Best Local Similarity	75.8%	Pred.	No. 6e-80				
Matches	659	Conservative	0	Mismatches	181	Indels	29
Gaps	5						
QY	102	GTGACATCCAGATGACATGCTCCAGCCTCCCTATCTGCATCTGTGGAGAAACTGCA	161				
	7	GGGACATTTTGATGACCAAGTATTCATCATCCCTGGCTGTGAGAAGGAGAGAAGTGA	66				
	162	CCATCACATGTCGGAGCAAGTGGGAATATTCAA	203				
	67	CTATGAGCTGCAAGTCAGTCAGAGTCTTTATGGAGTTGGAATCAAGAGAGCTGTTTAT	126				
	204	CATGGTATACAGACACACAGGAAAAATCTCTCAGCTCCTGTGTCTATTCTGCAAAAACCT	263				
Db	127	TCTGGCACCAAGAAAAACAGGCAGACTCTTAAACCACTGATCACTGGGCATCCAATA	186				
	264	TAGCAGATGGTGGCCATCAAGGTTTCAGTGGCAGTGGATCAGACACAAATATTTCTCTCA	323				
	187	GGGAACCTGGGGTCCCTGATCGCTTTTATAGGCAGTGGATCTGGAACAGATTTTACTCTCA	246				
	324	AGATTCAACAGCCTCGACGCTGAAGATTTTGGGAGTTTATTACTGTCAACATTTTTCGAGTA	383				
	247	CCATTAGCAGTATGCAGGCTGAAGATGTGGGTTTTTATTACTGTGAGCAGCATTTAGACA	306				
QY	384	CTCCGTACAGTTCCGAGGGGGGACCAAGCTGGAAATAAACGGGCTGATGCTGCACCAA	443				
	307	TTCCTT-CAGGTTTCGTTCCTGGGACCAAGCTGGAGATCAACGGGCTGATGCTGCACCA	365				
	444	CTGTATCCATCTTCCACACATCGATGAGCAGTTTAACTCTGGAGGTCCTCAGTCGTGT	503				
	366	CTGTATCTATCTTCCGCCCATCCACGGAAACAGTTAGCAACTGGAGGTCCTCAGTCGTGT	425				
	504	GCTTCTGTGAACAACTTCTACCCCAAGACATCAATGTCGAAGTGGAGATTTGATGGCAGTG	563				
Db	426	GCCTCATGAACAATCTCTATCCACAGACATCAGTGTCAAGTGGGAAGATTTGATGGCACTG	485				
	564	AAGCAAAAATGGCGTCTTGAAACGTTGGACTGTATCAGGACAGCAAAACAGACAGCTACA	623				
	486	AAGCAGGAGATGGTGTCTCTGGACAGTGTACTGTATCAGGACAGCAAAAGACAGCATACA	545				
	624	GCATGAGCAGCACCTCTCAGTTGACCAAGGACGAGTATGAACGACATTAACAGCTATACCT	683				
	546	GCATGAGCAGCACCTCTCTGTGTGACCAAGGCTTGACTATGAAAGTCATAACCTCTATACCT	605				
QY	684	GTGAGGCCACTCACAGACATCAACTTCACCCATTTGTCGAAGCTTCAACAGGAATGAGT	743				
	606	GTGAGGTGTTTATAGACATCATCTCACCGTGGTCAAGAGCTTCAACAGGAATGAGT	665				

Db 97 TCCATCATAGTAGGAGACAGGCTCAGCATCACCTGCAAGCCAGCAGTGTGGGTAT 156
QY 197 TATTAGATGTATCAGACAGACAGGAAATCTCTCAGCTCCTGGTCTATTTCTGCA 256
Db 157 GCTGTAGCCTGTGTATCAACAGAAACAGGCAATCTCTTAACTACTGATTTACTGGCA 216
QY 257 AAAACCTTAGCAGAGTGTGCTCCATCAAGTTTCAGTGGCAGTGGATCAGGAACAATAT 316
Db 217 TCCACCCGGCACACTGGAGTCTCTGATCGCTTCACAGGCAAGTGGATCTGGACAGATTTC 276
QY 317 TCTCTCAAGATCAACAGCCTCAGAGCTGAAGATTTGGGAGTTTACTGTCAACATTTT 376
Db 277 ACTCTCACCATTAGCAATGTGCAGTCTGAAGCTTGGGAGATTAATTTCTGTCAAGCAATAT 336
QY 377 TGGAGTACTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATTAACATCTGGAGTGTATGCT 436
Db 337 AGCAGCTATCGG---ACGTTGGTGGAGCACCAGCTGGAATTAACATCTGGAGTGTATGCT 393
QY 437 GCACCAACTGTATCCATCTCCACCATCTCAGTGAGCAGTTAAGCTTGGAGTGTATGCT 496
Db 394 GCACCAACTGTATCCATCTCCACCATCTCAGTGAGCAGTTAAGCTTGGAGTGTATGCT 453
QY 497 GTCGTGTCTTCTTCAACAACCTTACCCCAAGAGCAGTATGTAACATCTGGAGTGTATGCT 556
Db 454 GTCGTGTCTTCTTGAACAACCTTACCCCAAGAGCAGTATGTAACATCTGGAGTGTATGCT 513
QY 557 GGCAGTGAACACAAAATGGGCTCTGAACAGTTGGAGTGTATGTAACATCTGGAGTGTATGCT 616
Db 514 GGCAGTGAACACAAAATGGGCTCTGAACAGTTGGAGTGTATGTAACATCTGGAGTGTATGCT 573
QY 617 ACCTACAGCATGAGCAGCAGCCTCAGTTGACCAAGGAGCAGTATGTAACATCTGGAGTGTATGCT 676
Db 574 ACCTACAGCATGAGCAGCAGCCTCAGTTGACCAAGGAGCAGTATGTAACATCTGGAGTGTATGCT 633
QY 677 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCACTGTGTCAAGAGCTTCAACAGG 736
Db 634 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCACTGTGTCAAGAGCTTCAACAGG 693
QY 737 AATGAGTGTTA 747
Db 694 AATGAGTGTTA 704

RESULT 10

S-10-286-132A-22

Sequence 22, Application US/10286132A

GENERAL INFORMATION:

APPLICANT: Zhou, Tong

APPLICANT: Kimberly, Robert P.

APPLICANT: Koopman, William J.

APPLICANT: LoBuglio, Albert S.

APPLICANT: Buchsbaum, Donald J.

TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED

FILE REFERENCE: 21085.002907

CURRENT APPLICATION NUMBER: US/10/286,132A

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 60/346,402

PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: PCT/US01/14151

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/201,344

PRIOR FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.0

SEQ ID NO 22

LENGTH: 705

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct

S-10-286-132A-22

Query Match

Best Local Similarity 47.1%; Score 461.4; DB 9; Length 705;

Matches 547; Conservative 81.5%; Pred. No. 4.7e-78;

Mismatches 0; Indels 121; Gaps 1;

QY 77 CTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCAGTCTCAGGCTCCCTA 136

Db 37 CTGCTGTGGCTTACAGGTGTGAAGAGAGACATGTGTGATGACCCAGTCTCAAAATTCATG 96

QY 137 TCTGCATCTGTGGGAGAAACTGTCAACATCAATCTGCAGCAAGTGGGAAATATTTCAAAAT 196

Db 97 TCCACATCATAGTAGGAGACAGGCTCAGCATCACCTGCAAGGCCAGTCAAGGATGGGTACT 156

QY 197 TATTAGCATGTGTATCAGCAGACAGGGAATATCTCTCAGTCTCAGTCTCTGCTATTTCTGCA 256

Db 157 GCTGTAGCCTGTGTATCAACAGAAACAGGCAATCTCTTAACTACTGATTTACTGGGCA 216

QY 257 AAAACCTTAGCAGATGGTGTGCCATCAAGTTTCAGTGGCAGTGGATCAGGAACAATAT 316

Db 217 TCCACCCGGCACACTGGAGTCTCTGATCGCTTCACAGGCAAGTGGATCTGGACAGATTTC 276

QY 317 TCTCTCAAGATCAACAGCCTCAGAGCTTGAAGATTTTGGGAGTTTACTGTCAAAATTTT 376

Db 277 ACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATTAATTTCTGTCAAGCAATAT 336

QY 377 TGGAGTACTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATTAACATCTGGAGTGTATGCT 436

Db 337 AGCAGCTATCGG---ACGTTGGTGGAGCACCAGCTGGAATTAACATCTGGAGTGTATGCT 393

QY 437 GCACCAACTGTATCCATCTCCACCATCTCAGTGAGCAGTTAAGCTTGGAGTGTATGCT 496

Db 394 GCACCAACTGTATCCATCTCCACCATCTCAGTGAGCAGTTAAGCTTGGAGTGTATGCT 453

QY 497 GTCGTGTCTTCTTGAACAACCTTACCCCAAGAGCAGTATGTAACATCTGGAGTGTATGCT 556

Db 454 GTCGTGTCTTCTTGAACAACCTTACCCCAAGAGCAGTATGTAACATCTGGAGTGTATGCT 513

QY 557 GGCAGTGAACACAAAATGGGCTCTGAACAGTTGGAGTGTATGTAACATCTGGAGTGTATGCT 616

Db 514 GGCAGTGAACACAAAATGGGCTCTGAACAGTTGGAGTGTATGTAACATCTGGAGTGTATGCT 573

QY 617 ACCTACAGCATGAGCAGCAGCCTCAGTTGACCAAGGAGCAGTATGTAACATCTGGAGTGTATGCT 676

Db 574 ACCTACAGCATGAGCAGCAGCCTCAGTTGACCAAGGAGCAGTATGTAACATCTGGAGTGTATGCT 633

QY 677 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCACTGTGTCAAGAGCTTCAACAGG 736

Db 634 TATACCTGTGAGGCCACTCACAAGACATCACTTCAACCACTGTGTCAAGAGCTTCAACAGG 693

QY 737 AATGAGTGTTA 747

Db 694 AATGAGTGTTA 704

RESULT 11

US-10-281-479A-22

Sequence 22, Application US/10281479A

GENERAL INFORMATION:

APPLICANT: The UAB Research Foundation

APPLICANT: Zhou, Tong

APPLICANT: Ichikawa, Kimihisa

APPLICANT: Kimberly, Robert P.

APPLICANT: Koopman, William J.

APPLICANT: Oshumi, Jun

APPLICANT: LoBuglio, Albert S.

APPLICANT: Buchsbaum, Donald J.

TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS

TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T

TITLE OF INVENTION: AGENTS

FILE REFERENCE: 21085.002906

CURRENT APPLICATION NUMBER: US/10/281,479A

CURRENT FILING DATE: 2003-01-28

PRIOR APPLICATION NUMBER: 60/391,478

80 CTCAGCTCTTTGGCTGTCTCTTAGGGCAGAGGGCCACCATCTCTGCAAGGCCAGCC 139
183 GGAATATTCAAAA-----TTATTAGCATGGTATCAGGACACACAGGAAAT 230
140 AAAGTGTGTTATGATGGTGATAGTTTATATGAACCTGTACCAACAGAAACAGGACAGC 199
231 CTCTCAGCTCCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
200 CACCAAACTCCCTCATCTATGCTGCATCCCAATCTAGAACTGGGATCCAGCCAGGTTTA 259
291 GTGCGATGGATCAGGAACAATAATTCTCTCAAGATCAACAGCCTCGAGCCTGAAGATT 350
260 GTGCACTGGTCTGGGACAGACTTCAACCTCAACATCCATCTCTGTGGAGGAGGAGATG 319
351 TTGGGAGTTATTAAGTGTCAACATTTTGGAGTACTCCGTACAGCTTCGGAGGGGGACCA 410
320 CTGCAACCTATTACTGTCAAGAAAGTAATGAGGATCCTCGGACGTTCCGGTGGAGGCCCA 379
411 AGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTG 470
380 AGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTG 439
471 AGCAGTTAAACATCTGGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAG 530
440 AGCAGTTAAACATCTGGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAG 499
531 ACATCAATGTCAAGTGGAGATTTGATGGCAGTGAACGACAAATGGGCTCTGCAACAGTT 590
500 ACATCAATGTCAAGTGGAGATTTGATGGCAGTGAACGACAAATGGGCTCTGCAACAGTT 559
591 GGACTGTACGAGCAGCAAGACAGCAGCTACAGCATGAGCAGCACCTCAGTTTGACCA 650
560 GGACTGTACGAGCAGCAAGACAGCAGCTACAGCATGAGCAGCACCTCAGTTTGACCA 619
651 AGGAGGATGTGACGAGCATACAGCTATACCTGTGAGGCCACTCACAGACATCAACTT 710
620 AGGAGGATGTGACGAGCATACAGCTATACCTGTGAGGCCACTCACAGACATCAACTT 679
711 CACCATTTGTCAAGAGCTTCAACAGGAATGAGTGT 745
680 CACCATTTGTCAAGAGCTTCAACAGGAATGAGTGT 714

:SULT 15

S-10-251-215-47

Sequence 47, Application US/10251215

GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.

APPLICANT: Kretz-Rommel, Anke

APPLICANT: Frederickson, Shana

TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED

FILE OF INVENTION: 1087-36

FILE REFERENCE: 1087-36

CURRENT APPLICATION NUMBER: US/10/251,215

CURRENT FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US 60/323,537

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/323,544

PRIOR FILING DATE: 2001-09-20

PRIOR APPLICATION NUMBER: US 60/379,980

PRIOR FILING DATE: 2002-05-13

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin version 3.2

SEQ ID NO 47

LENGTH: 702

TYPE: DNA

ORGANISM: murine

S-10-251-215-47

Query Match

Best Local Similarity 45.5%; Score 445.2; DB 8; Length 702;

Matches 522; Conservative 2; Mismatches 110; Indels 2; Gaps 1;

Qy 112 GATGACTCAGTCTCCAGCCCTCCCTATCTGTCATCTGTGGAGAAACTGTCCACCATCATCATG 171
Db 15 GCTCACCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACCATAACTG 74
Qy 172 TCAGAGCAAGTGGGAATATTCAAAATTTATTAGCATGGTATATCAGCAGACACAGGAAATC 231
Db 75 C--AACTGCCAGCTCAAGTGTAAAGTACATGCACCTGGTTCAGCAGAAAGCCAGGACCTTC 132
Qy 232 TCCTCAGCTCTCTGGTCTATTCTGCAAAAACCTTTAGCAGATGGTGTGCCATCAAGGTTCA 291
Db 133 TCCCAAACTCTTGATTTATAGCRCATCAACCTGGCTTCTGGAGTCCCTGCTGCTCTTCAG 192
Qy 292 TGGCAGTGGATCAGGAACAATAATTCTCTCAAGATCAACAGCCTGGAGCCTGAAGATTT 351
Db 193 TGGCAGTGGATCTGGGACCTCTTACTCTCTCAAAATCAGCCGAATGGAGGCTGAAGATGC 252
Qy 352 TGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACACAGTTTCGGAGGGGGACCAA 411
Db 253 TGGCAGTTATTACTGTCCAGCAAGAGGATAGTTACCCATGGAGCTTCGGTGGAGGCCAA 312
Qy 412 GCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGA 471
Db 313 GCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGA 372
Qy 472 GCAGTTAACATCTGAGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAGA 531
Db 373 GCAGTTAACATCTGAGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAGA 432
Qy 532 CATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAATGGGCTCTGCAACAGTTG 591
Db 433 CATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAATGGGCTCTGCAACAGTTG 492
Qy 592 GACTGATCAGGACAGCAAGAGCAGCAGCCTACAGCATGAGCAGCACCTCAGCTTGACCAA 651
Db 493 GACTGATCAGGACAGCAAGAGCAGCAGCCTACAGCATGAGCAGCACCTCAGCTTGACCAA 552
Qy 652 GGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAGACATCAACTTC 711
Db 553 GGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAGACATCAACTTC 612
Qy 712 ACCCATTTGCAAGAGCTTCAACAGGAATGAGTGTTA 747
Db 613 ACCCATTTGCAAGAGCTTCAACAGGAATGAGTGTTA 648

Search completed: June 24, 2003, 01:56:54

Job time : 786.157 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 18:59:37 ; Search time 2450.36 Seconds
(without alignments)
10045.255 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 acacccttgctgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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27: /cgn2_6/ptodata/1/pna/US096D_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*
31: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*
32: /cgn2_6/ptodata/1/pna/US098A_COMB.seq.*
33: /cgn2_6/ptodata/1/pna/US098B_COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*
36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq.*
39: /cgn2_6/ptodata/1/pna/US100A_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US100B_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US101A_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US101B_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq.*
44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	100.0	979	100.0	979	30	US-09-770-916-3	Sequence 3, Appli
2	769.6	78.6	937	8	US-08-480-120-3	Sequence 3, Appli	Sequence 13035, A
3	733.6	74.9	998	1	PCT-US02-25766-13035	Sequence 3, Appli	Sequence 1, Appli
4	708.6	72.4	751	4	US-08-090-534-3	Sequence 5, Appli	Sequence 8, Appli
5	693.4	70.8	1041	3	US-07-904-074A-1	Sequence 8, Appli	Sequence 13, Appli
6	693.4	70.8	1041	3	US-07-904-074A-5	Sequence 8, Appli	Sequence 4, Appli
7	634.2	64.8	5711	33	US-09-897-006-8	Sequence 13, Appli	Sequence 4, Appli
8	634.2	64.8	5711	33	US-09-897-511A-8	Sequence 4, Appli	Sequence 4, Appli
9	634.2	64.8	6255	33	US-09-897-006-13	Sequence 4, Appli	Sequence 4, Appli
10	634.2	64.8	6255	33	US-09-897-511A-13	Sequence 4, Appli	Sequence 4, Appli
11	615.6	62.9	943	3	US-07-733-329-4	Sequence 4, Appli	Sequence 4, Appli
12	615.6	62.9	943	7	US-08-303-569-4	Sequence 4, Appli	Sequence 4, Appli
13	615.6	62.9	943	8	US-08-415-686-4	Sequence 4, Appli	Sequence 4, Appli
14	615.6	62.9	943	12	US-08-46-658A-4	Sequence 4, Appli	Sequence 4, Appli
15	615.6	62.9	943	12	US-08-46-658B-4	Sequence 4, Appli	Sequence 4, Appli
16	615.6	62.9	943	17	US-09-48-224-4	Sequence 4, Appli	Sequence 4, Appli
17	615.6	62.9	943	30	US-09-95-515-4	Sequence 4, Appli	Sequence 4, Appli
18	598	61.1	882	8	US-08-412-767-3	Sequence 3, Appli	Sequence 386, App
19	594.8	59.7	764	60	US-60-168-599-386	Sequence 21147, A	Sequence 5847, Ap
20	576.6	58.9	2221	80	US-60-160-207-21147		
21	558.8	57.1	709	29	US-09-724-671-5847		

22	535	54.6	831	23	US-09-613-017-3	Sequence 3, Appl
23	535	54.6	831	34	US-09-903-327A-3	Sequence 3, Appl
24	504.2	51.5	671	29	US-09-724-671-10262	Sequence 10262, A
25	483.2	49.4	724	16	US-09-237-061-1	Sequence 1, Appl
26	482.6	49.3	633	4	US-08-070-160-7	Sequence 7, Appl
27	482.6	49.3	633	7	US-08-373-297-7	Sequence 7, Appl
28	476.6	48.7	746	3	US-07-688-197-1	Sequence 1, Appl
29	476	48.6	1106	1	PCT-US01-19569-121	Sequence 121, App
30	476	48.6	1106	43	US-10-464-049-121	Sequence 121, App
31	461.4	47.1	705	1	PCT-US01-14151-22	Sequence 22, Appl
32	460.2	47.0	1066	5	US-08-157-101-4	Sequence 4, Appl
33	459	46.9	476	29	US-09-724-671-7170	Sequence 7170, Ap
34	459	46.9	944	23	US-09-602-148A-48	Sequence 48, Appl
35	458.8	46.9	723	7	US-08-350-400-56	Sequence 56, Appl
36	458.8	46.9	723	8	US-08-350-400A-56	Sequence 56, Appl
37	458.8	46.9	723	8	US-08-467-175-56	Sequence 56, Appl
38	458.8	46.9	723	8	US-08-467-175A-56	Sequence 56, Appl
39	458.8	46.9	723	8	US-08-467-564-56	Sequence 56, Appl
40	457.6	46.7	974	30	US-09-760-479-192	Sequence 192, App
41	457.6	46.7	974	42	US-10-206-008-192	Sequence 9, Appl
42	453.8	46.4	678	18	US-09-454-925A-9	Sequence 29, Appl
43	453.2	46.3	974	32	US-09-859-053-29	Sequence 18, Appl
44	453	46.3	698	38	US-10-006-773-18	Sequence 21, Appl
45	452	46.2	738	17	US-09-338-321A-21	Sequence 18, Appl

ALIGNMENTS

SULT 1
-09-770-916-3
Sequence 3, Application US/09770916
GENERAL INFORMATION:
APPLICANT: Frank, Dara W.
APPLICANT: Wiener-Kronish, Jeannine
APPLICANT: Yahr, Timothy L.
APPLICANT: Sawa, Teiji
TITLE OF INVENTION: Method of and compositions for immunization with the
TITLE OF INVENTION: pseudomonas v antigen
FILE REFERENCE: 650053.91487
CURRENT APPLICATION NUMBER: US/09/770,916
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/448,339
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/109,952
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/126,794
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 979
TYPE: DNA
ORGANISM: mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (44)..(745)
NAME/KEY: sig_peptide
LOCATION: (44)..(103)
NAME/KEY: V_region
LOCATION: (104)..(172)
OTHER INFORMATION: FR1
NAME/KEY: V_region
LOCATION: (173)..(205)
OTHER INFORMATION: CDR1
NAME/KEY: V_region
LOCATION: (206)..(250)
OTHER INFORMATION: FR2
NAME/KEY: V_region
LOCATION: (251)..(271)
OTHER INFORMATION: CDR2
NAME/KEY: V_region

QY 266 GCAGATGGTGGCCATCAAGTTTCAGTGGCAGTGGATCAGGAACACAAATATCTCTCAAG 325
Db 255 GCAGATGGTGGCCGTCAGTTTCAGTGGCAGTGGATCAGGAACACAAATATCTCTCAAG 314
QY 326 ATCAACAGCCTGCAGCCTGAAGATTTTGGAGTTTACTGTCAACATTTTGGAGTACT 385
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QY 386 CCGTACACCTTCCGAGGGGGGACCAAGCTGGAATTAACACGGGCTGATGTCACCAACT 445
Db 375 CCGTACACCTTCCGAGGGGGGACCAAGCTGGAATTAACACGGGCTGATGTCACCAACT 434
QY 446 GTATCCATCTTCCCACTCAGTGGAGCTTAACATCTGGAGGTCCTCAGTCGTGTGC 505
Db 435 GTATCCATCTTCCCACTCAGTGGAGCTTAACATCTGGAGGTCCTCAGTCGTGTGC 494
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Db 555 GCACAAATATGGGCTCCTGAACAGTTGGAGTATCAGGACAGCAAAAGACAGCACTACAGC 614
QY 626 ATGACGACGACCTCAGCTTGACCAAGGACAGTATGAACGACATTAACAGCTATACCTGT 685
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746 TAG 748
735 TAG 737

RESULT 5

Sequence 1, Application US/07904074A-1
GENERAL INFORMATION:
APPLICANT: John E. Shively
APPLICANT: Rainer Fischer
APPLICANT: Anna Wu
APPLICANT: Roy Paxton
APPLICANT: Y.H. Joy Yang
TITLE OF INVENTION: Chimeric Anti-CEA Antibody
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte
STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPUTER READABLE FORM:
COMPUTER: Wang PC
OPERATING SYSTEM: MS-DOS (R) Version 3.30
SOFTWARE: Microsoft (R)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/904,074A
FILING DATE: 19920615
CLASSIFICATION: 530
PRIOR APPLICATION DATA: None
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: None
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 785-6938
TELEFAX: (202) 785-5351
TELEX: 440087 LM WSH

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1041
TYPE: NUCLEIC ACID
STRANDEDNESS: Single Stranded
TOPOLOGY: Unknown
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: Not Applicable
ANTI-SENSE: Not Applicable
FRAGMENT TYPE: Not Applicable
ORIGINAL SOURCE: Synthetically Prepared
IMMEDIATE SOURCE: Synthetically Prepared
POSITION IN GENOME: None
FEATURE: None
PUBLICATION INFORMATION: None
US-07-904-074A-1

Query Match 70.8%; Score 693.4; DB 3; Length 1041;
Best Local Similarity 85.0%; Pred. No. 4e-86;
Matches 788; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
QY 56 ACTCAGTCTCTGGCGTTGCTGCTGTGCTGTACAGTGGCCAGATGTGACATCCAGATG-115
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QY 176 GCAAGTGGAAATTCAAATTTATTTAGCATGGTATCAGCAGACACAGGAAATCTCT 235
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QY 236 CAGTCTCTGCTATCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGC 295
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QY 473 CAGTTAATCTGGAGGTCCTCAGTCTGTGCTTCTTTGAAACAACTTACCCCAAGAC 532
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Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;

CORRESPONDENCE ADDRESS:

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SULT 15

RESULT 15
US-08-846-658B-4
Sequence 4. Application US/08846658B

GENERAL INFORMATION.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846, 655B
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057

REFERENCE/DOCKET NUMBER:

TELEPHONE: (215) 568-3100

TELEPHONE: (215) 568-3439
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 943 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: 11near

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 18..722

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 84..722
US-08-846-658B-4

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Query Match          62.9%; Score 615.6; DB 12; Length 943;
Best Local Similarity 84.6%; Pred. No. 2e-75;
Matches 739; Conservative 0; Mismatches 129; Indels 6;

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[illegible]

Search completed: June 24, 2003, 00:11:44
Job time : 2455.36 secs

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2641 ATCAGGACACAAATATTCTCTCAGATCAACAGCTCCAGCTGAAGATTTTGGGAGTTA 2700
361 TTACTGTCAACATTTTGGAGTACTCGGTACACGTTCCGAGGGGGACCAAGCTGGAAAT 420
2701 TTACTGTCAACATTTTGGAGTACTCGGTACACGTTCCGAGGGGGACCAAGCTGGAAAT 2760
421 AAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCAATCCAGTGAGCAAGTTAA 480
2761 CAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCAATCCAGTGAGCAAGTTAA 2820
481 ATCTGGAGTGCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAATGT 540
2821 ATCTGGAGTGCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAATGT 2880
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721 CAAGAGCTTCAACAGGAATGAGTTGAGAGCAAAAGTCTTGAGAGCCGACCAAGCAGTCT 780
3061 CAAGAGCTTCAACAGGAATGAGTTGAGAGCAAAAGTCTTGAGAGCCGACCAAGCAGTCT 3120
781 CCCAGCTCCATCTATCTTCCT 803
3121 CCTCCCCCCCCCTTAACGTTACT 3143

RESULT 2

3-09-897-006-8
Sequence 8, Application US/09897006
Patent No. US20020106729A1
GENERAL INFORMATION:

APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Expression Vectors
FILE REFERENCE: GALA-06415
CURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 5711
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic

3-09-897-006-8

Query Match 64.8%; Score 634.2; DB 10; Length 5711;
Best Local Similarity 90.8%; Pred. No. 1.3e-156;
Matches 675; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
61 GGTCTGGGTTTGGTCTGCTGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA 120
2401 GGTCTTTCTCTTCTCTCTCTCAGTAACTACAGGTGTCCACTCCGACATCCAGATGACCA 2460
121 GTCCTCAGCTCCCTATCTGCTGCTGGAGAACTGTGAGCAATCAGATGCTGAGCAAG 180
2461 GTCTCAGCTCCCTATCTGCTGCTGGAGAACTGTGAGCAATCAGATGCTGAGCAAG 2520

QY 181 TGGGAATATTCAAAATTTATTAGCATGTTATCAGCAGACACAGGAAAAATCTCTCAGCT 240
DB 2521 TGGGAATATTCAAAATTTATTAGCATGTTATCAGCAGAAACAGGAAAAATCTCTCAGCT 2580
QY 241 CCTGGTCTATTCTCAAAAACCTTAGCAGATGTTGTGCCATCAAGTTTTCAGTGGCAGTGG 300
DB 2581 CCTGGTCTATAATGCAAAAACCTTAGCAGATGTTGTGCCATCAAGTTTTCAGTGGCAGTGG 2640
QY 301 ATCAGGACACAAATATTCTCTCAGATCAACAGCTCCAGCTGAAGATTTTGGGAGTTA 360
DB 2641 ATCAGGACACAAATATTCTCTCAGATCAACAGCTCCAGCTGAAGATTTTGGGAGTTA 2700
QY 361 TTACTGTCAACATTTTGGAGTACTCGGTACACGTTCCGAGGGGGACCAAGCTGGAAAT 420
DB 2701 TTACTGTCAACATTTTGGAGTACTCGGTACACGTTCCGAGGGGGACCAAGCTGGAAAT 2760
QY 421 AAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCAATCCAGTGAGCAAGTTAA 480
DB 2761 CAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCAATCCAGTGAGCAAGTTAA 2820
QY 481 ATCTGGAGTGCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAATGT 540
DB 2821 ATCTGGAGTGCCTCAGTCGCTGCTTCTTGAACAACATTTACCCCAAGACATCAATGT 2880
QY 541 CAAGTGAAGATTGATGGCAGTGAACGACAAATGGCGTCTGAACAGTTGGACTGATCA 600
DB 2881 CAAGTGAAGATTGATGGCAGTGAACGACAAATGGCGTCTGAACAGTTGGACTGATCA 2940
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DB 2941 GGACAGCAAAAGACAGCAGCTACAGCATGAGCAGCACCCTCAGTTGACCAAGGAGGAGTA 3000
QY 661 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCAACCATTTGT 720
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QY 721 CAAGAGCTTCAACAGGAATGAGTTGAGAGCAAAAGTCTTGAGAGCCGACCAAGCAGTCT 780
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QY 781 CCCAGCTCCATCTATCTTCCT 803
DB 3121 CCTCCCCCCCCCTTAACGTTACT 3143

RESULT 3

US-09-897-511A-13
; Sequence 13, Application US/09897511A
; Publication NO. US20030092882A1
; GENERAL INFORMATION:
; APPLICANT: Bremel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 6255
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-13

Query Match 64.8%; Score 634.2; DB 9; Length 6255;
Best Local Similarity 90.8%; Pred. No. 1.4e-156;
Matches 675; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

[illegible]

<p> RESULT 8 US-09-859-053-29 ; Sequence 29, Application US/09859053 ; Patent No. US20020102658A1 ; GENERAL INFORMATION: ; APPLICANT: Tsuji, Takashi ; APPLICANT: Tezuka, Katsunari ; APPLICANT: Hori, No. US20020102658A1uaki ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A ; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND ; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF ; FILE REFERENCE: 06501-079001 ; CURRENT APPLICATION NUMBER: US/09/859,053 ; CURRENT FILING DATE: 2001-05-16 ; PRIOR APPLICATION NUMBER: JP 2001-99508 ; PRIOR FILING DATE: 2001-03-30 ; PRIOR APPLICATION NUMBER: JP 2000-147116 ; PRIOR FILING DATE: 2000-05-18 ; NUMBER OF SEQ ID NOS: 43 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 29 ; LENGTH: 974 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: </p>	
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QY	161	ACCATCATGTCTGAGCAAGTGGGAATATTCAAAATTTATTACATGGTATCAGCAGACA	220
Db	125	ACCATCACTTGGCAGGGAGTCAAGACATCGCAACTATTGAAATGGTATCAGCAGAA	184
QY	221	CAGGAAATCTCCTCAGCTCCCTGGTCTATTCTGCAAAAACCTTAGCATGGTGTGCCA	280
Db	185	CCGGGAAACCCCAAACTCTGTATCTTCGATGGATCTATTTTACATACAGGGTCCCA	244
QY	281	TCAAGGTTTCACTGGCAGTGGATCAGGAACACAAATATCTCTCAAGATCAACAGCTGCAG	340
Db	245	TCAAGGTTTCACTGGAGTGGATCTGGGACACATTTCACTTTCAACATCAACAACCTGCAG	304
QY	341	CCTTGAAGATTTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACAGTTCGGA	400
Db	305	CCTGACGATTTTCAACATATTCCTGTCAACARTATAATACITTCCTCCCTCACTTCGGC	364
QY	401	GGGGGACCAAGCTGAAATATAACCGGCTGATGCTGCACCAACTGTATCCATCTTCCCA	460
Db	365	SRAGGACCAAGTGGARATCAACAACTGTGGTGCACCATCTGTCTCATCTTCCCG	424
QY	461	CCATCAGCTGAGCAGTTAACTCTGGAGTGGCTCAGTCGTCTGTCTTCTTGAACAATTC	520
Db	425	CCATCTGATGAGCGTTGAAATCTGGAATCGCCTCTGTGTGTGCTCTGCTGAATAACTTC	484
QY	521	TACCCCAAGACATCAATCTCAAGTGGAAAGATTGATGCGAGTGAACGACAAATGGCGTC	580
Db	485	TATCCAGAGGCCAAGTACAGTGGAAAGTGGATTAAGCCCTCCAATCGGGTAACTCC	544
QY	581	CTGAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATCAGCAGCACCTC	640
Db	545	CAGGAGAGTGTACAGAGCAGGACAGCAAGGACACCTACAGCCTCAGCAGCACCTG	604
QY	641	ACGTTCAACAAGCAGTATGAACGACATTAACGCTATACCTGTGAGGCCACTCACAAG	700
Db	605	ACGCTGAGCAAAAGCAGACTACGAGAAAACACAAAGTCTACGCCCTCGAAGTCAACCATCAG	664
QY	701	ACATCAACTTCAACCATTTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGCAAAAGTCC	760
Db	665	GGCTGAGTCCCGCTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGGAGAGAAGTGC	724
QY	761	TGAGACGCCACACACGCTCCCAAGCTCCATCTTATCTTCCCTTCTAAGGTCCTGGAGGC	820
Db	725	CCCCACCTGCTCCTCAGTTCAGCTGACCTGACCCCTCCCATCTTT---GGCCTGTGACCT	781
QY	821	TTTCCCAACAGGACCTACCACTGTGCGGTGCTCCAAACCTCTCTCCCACTCTCTCTC	880
Db	782	TTTTTCCACAGGGGACCTACCCCTATTGGGGTCTCCA-----GCTCATCTTTCACTC	834
QY	881	CTCCTCTCCTTTCCTTGGCTTTTATCATGCTTAATATTTGCAGAAAT-ATTCAATAAA	939
Db	835	ACCCCTCTCTCTCTCTTGGCTTTAAATATGCTAATGTTGGAGGAGAAATCAATAATAAA	894
QY	940	GTGAGTCTTTTGCAAAAAATAAAAAAAAAAAAAAAAAAAAAA	979
Db	895	GTGAATCTTTGCANAAAAAATAAAAAAAAAAAAAAAAAAAAAA	934

RESULT 14

\$-09-897-511A-11
Sequence 11, Application US/09897511A
Publication No. US20030092882A1

GENERAL INFORMATION:
APPLICANT: Bremei Robert

AFFILIANT: BIELETT, ROBERT
APPLICANT: MILLER, LINDA

APPLICANT: Black, Gregory

TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors

```

; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; IS-09-897-511A-11

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Query Match 43.9%; Score 430; DB 9; Length 5691;
Best Local Similarity 80.2%; Pred. No. 7e-103;
Matches 531; Conservative 0; Mismatches 125; Indels 6; Gaps 2;

104	QY	GACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGCACTCTGGGAGAAACTGTCA	163
3800	Db ₁	GACATTGTGTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC	3859
164	QY	ATCACAATGTCGAGCAGTGGGAATATTCAAAATATTATAGCATGGTATCAGACACACAG	223
3860	Db ₂	ATGACCTGCAGTGGCCACCTTCAAGTGT---AAGTTACATACACTGGTACCAGCAGAAGTCA	3916
224	QY	GGAAAATTCCTTCAGTCTCCTGCTCATTTCTGCAAAACCTTAGCAGATGGTGTGCCATCA	283
3917	Db ₃	GGCACTCCCCAAAGATGGAATTTATGACATCCAAACTGGCTTCGGAGTCCCTGCT	3976
284	QY	AGGTTCACTGGCAGTGGATCAGGAACACAAATATCTCAAGATCAACAGCTGCGAGCCT	343
3977	Db ₄	CGCTTCAGTGGCAGTGGGTCTGGGACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCT	4036
344	QY	GAAGATTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACAGTTTCGGAGGG	403
4037	Db ₅	GAAGATGCTGCCACTTATTACTTGCCAGCA---GTGGGGTAGTTACCTCACGTTGGGTGG	4093
404	QY	GGGACCAGCTGGAAATTAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	463
4094	Db ₆	GGGACCAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA	4153
464	QY	TCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGNACAACTTCTAC	523
4154	Db ₇	TCCAGTGAGCAGTTAACATCTGGAGGTGCCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC	4213
524	QY	CCCAAGACATCAATGTCAAGTGGAAABATTGATGGCAGTGAACGACAAAATGGCGTCTGTG	583
4214	Db ₈	CCCAAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACGACAAAATGGCGTCTGTG	4273
584	QY	AACAGTTGGACTGATCAGGACAGCAAGACAGCACCTTACAGCATGAGCAGCACCCCTCAG	643
4274	Db ₉	AACAGTTGGACTGATCAGGACAGCAAGACAGCACCTTACAGCATGAGCAGCACCCCTCAG	4333
644	QY	TTGACCAGGACGAGTATGACGACATTAACAGCTTATACCTGTGAGGCCACCTCACAGACA	703
4334	Db ₁₀	TTGACCAGGACGAGTATGACGACATTAACAGCTTATACCTGTGAGGCCACCTCACAGACA	4393
704	QY	TCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCTCTGA	763
4394	Db ₁₁	TCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGAGAGATCTCGA	4453
764	GA	765	
4454	CA	4455	

RESULT 15

US-09-897-006-11
; Sequence 11, Application US/09897006
; Patent No. US2020106729A1
; GENERAL INFORMATION:

APPLICANT: Black, Gregory					
TITLE OF INVENTION: Expression Vectors					
FILE REFERENCE: GALA-06415					
CURRENT APPLICATION NUMBER: US/09/897,006					
CURRENT FILING DATE: 2001-06-29					
PRIOR APPLICATION NUMBER: 60/215,851					
PRIOR FILING DATE: 2000-07-03					
NUMBER OF SEQ ID NOS: 36					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 11					
LENGTH: 5691					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Synthetic					
-09-897-006-11					
Query Match 43.9%; Score 430; DB 10; Length 5691;					
Best Local Similarity 80.2%; Pred. No. 7e-103;					
Matches 531; Conservative 0; Mismatches 125; Indels 6; Gaps 2;					
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3800	GACATTGCTGCACACAATCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGTGTCACC	3859			
164	ATCACATGTCGGAACAAGTGGGAATATTCAAATAATTATTAGCATGTTATCACGACACACAG	223			
3860	ATGACCTGTCAGTGCCACCTCAAGTGT---AGTTATACATACACTGGTAGCCAGCAGAAGTCA	3916			
224	GGAAATCTCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCA	283			
3917	GGCACCTCCCCCAAAAGATGGATTATGACACATCCAACACTGGCTTCGGATCCCTGCT	3976			
284	AGTTTCAGTGGCAGTGGATCAGGAACAACAATATTTCTCAAGATCAACAGCCTCGAGCCT	343			
3977	CGTTTCAGTGGCAGTGGTCTGGGACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCT	4036			
344	GAAGATTTTGGGAGTTATTAATCTGTCAACATTTTGGAGTACTCCGTACACGTTCCGGGG	403			
4037	GAAGATGCTGCCACTTATTACTGCCAGCA---GTGGGGTAGTTACCTCAGTTCGGTGGC	4093			
404	GGGACCAAGCTGGAAATAAACAACGGCTGATGCTGCACCAACTGTATCCCATTTCCACCA	463			
4094	GGGACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTCCACCA	4153			
464	TCCAGTGAGCAGTTTAACATCTGGAGTGGCTCAGTGGTGTCTTGTAAACAATCTTAC	523			
4154	TCCAGTGAGCAGTTAACATCTGGAGTGGCTCAGTGGTGTCTTGTAAACAATCTTAC	4213			
524	CCCAAGACATCAATGTCAAGTGGGAAGATTGATGGCAGTGAACGACAAAAATGGCGTCTG	583			
4214	CCCAAGACATCAATGTCAAGTGGGAAGATTGATGGCAGTGAACGACAAAAATGGCGTCTG	4273			
584	AACAGTTGGACTGATCAGGACACAAAGACAGCACCTTACAGCATGAGCAGCACCTTCAG	643			
4274	AACAGTTGGACTGATCAGGACACAAAGACAGCACCTTACAGCATGAGCAGCACCTTCAG	4333			
644	TTGACCAAGGACGAGTATGAACGACATAACAGCTATATACCTGTGAGGCCACTCACAAGCA	703			
4334	TTGACCAAGGACGAGTATGAACGACATAACAGCTATATACCTGTGAGGCCACTCACAAGCA	4393			
704	TCAACTTCCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGA	763			
4394	TCAACTTCCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGA	4453			
764	GA 765				
4454	CA 4455				

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:18:11 ; Search time 51.8675 Seconds
(without alignments)
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Title: US-09-770-916-3

Perfect score: 979

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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3: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	708.6	72.4	751	5	PCT-US94-07659-3
2	667.6	68.2	927	2	US-07-690-192-1
3	650.6	66.5	940	1	US-08-353-400-24
4	626	63.9	1644	2	US-08-792-824-11
5	626	63.9	1672	2	US-08-792-824-2
6	626	63.9	4435	2	US-08-792-824-1
7	622.8	63.6	1632	2	US-08-792-824-8
8	615.6	62.9	943	2	US-08-303-569B-4
9	615.6	62.9	943	2	US-08-116-247-4
10	597.2	61.0	1641	2	US-08-792-824-5
11	517.2	52.8	642	2	US-08-634-783A-2
12	517.2	52.8	642	2	US-09-070-817-2
13	509.6	52.1	652	2	US-08-737-129A-7
14	485.8	49.6	5238	6	5453363-1
15	482.6	49.3	633	4	US-09-170-769A-7
16	460.2	47.0	1066	1	US-08-157-101A-4
17	459.2	46.9	714	3	US-09-192-545-3
18	458.8	46.9	723	5	PCT-US94-14106-56
19	449.4	45.9	732	2	US-08-860-882A-26
20	449.4	45.9	732	4	US-09-423-439-57
21	449.4	45.9	732	4	US-09-011-769A-22
22	436.8	44.6	648	6	5455030-4
23	432.8	44.2	646	2	US-08-737-129A-3
24	432	44.1	3819	4	US-09-042-353-393
25	432	44.1	3819	4	US-08-758-417A-243
26	422.2	43.1	645	4	US-09-170-769A-3
27	411	42.0	723	5	PCT-US94-14106-60

28 407.6 41.6 19040 4 US-09-343-485A-3 Sequence 3, Appli
29 393.8 40.2 726 4 US-08-487-283A-9 Sequence 9, Appli
30 389.8 39.8 1443 2 US-08-403-853-19 Sequence 19, Appli
31 384.4 39.3 705 1 US-08-488-376-16 Sequence 16, Appli
32 384.4 39.3 705 2 US-08-634-223-16 Sequence 16, Appli
33 384.4 39.3 705 2 US-08-634-224-16 Sequence 16, Appli
34 384.4 39.3 705 2 US-08-634-400-16 Sequence 16, Appli
35 384.4 39.3 705 2 US-08-635-878-16 Sequence 16, Appli
36 384.4 39.3 705 2 US-08-770-057-16 Sequence 16, Appli
37 384.4 39.3 705 4 US-09-335-697B-16 Sequence 16, Appli
38 384.4 39.3 705 4 US-09-335-697B-16 Sequence 19, Appli
39 382.6 39.1 931 3 US-09-049-672A-19 Patent No. 5219996
40 378.2 38.6 420 6 5219996-18 Sequence 5, Appli
41 376.4 38.4 472 2 US-08-579-940-5 Sequence 15, Appli
42 365.6 37.3 711 4 US-08-487-283A-15 Sequence 18, Appli
43 365.2 37.3 708 1 US-08-488-376-18 Sequence 18, Appli
44 365.2 37.3 708 2 US-08-634-223-18 Sequence 18, Appli
45 365.2 37.3 708 2 US-08-634-224-18 Sequence 18, Appli

ALIGNMENTS

RESULT 1
PCT-US94-07659-3
; Sequence 3, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurler, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized 11-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of 11-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

[illegible]

RESULT 3

US-08-353-400-24
Sequence 24, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 940 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-353-400-24

Query Match	66.5%;	Score 650.6;	DB 1;	Length 940;
Best Local Similarity	83.8%;	Pred. No. 1.6e-147;		
Matches 780;	Conservative 0;	Mismatches 129;	Indels 22;	Gaps 3;
39	CAGTCATGAGTGTGCTC	CACTCAGGTCC	TGGCGTTCGTCGTCGTGTCGTCGTACAGGTGCCA	98
5	CCGCGATGGATTCACAG	CGCCCGCTTTATATTGCTGCTATGGTATCTGGAACT	64	
99	GATGTGACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGCATGTGTGGGAGAACTG	158		
65	GTGGGACATTTGATGTACAGTCTCCATCTCCCTCCCTGCTGTGTGTCAGCAGGAGACAGG	124		
159	TCACCATCATGTGCGAGCAAGTGGGAATATTC-----	200		
			-----	AAAAATTATT

[illegible]

RESULT 4

US-08-792-824-11
: Sequence 11, Application US/08792824
: Patent No. 5932449
: GENERAL INFORMATION:
: APPLICANT: EMANUEL, PETER A.
: APPLICANT: BURANIS, JAMES P.
: APPLICANT: VALDES, JAMES J.
: APPLICANT: MOHYEE, ELDEFRAWI E.
: TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: U.S. Army Chemical and Biological Defense
: ADDRESSEE: Command
: STREET: Office of the Chief Counsel, Bldg E4435
: CITY: Aberdeen Proving Ground
: STATE: MD

Query Match	63.9%;	Score 626;	DB 2;	Length 1672;
Best Local Similarity	92.9%;	Pred. No. 1.5e-141;		
Matches	656;	Conservative 0;	Mismatches 50;	Indels 0;
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111	AGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAACTGTCCACATCACAT	170		
190	AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAACTGTCCACATCACAT	249		
171	GTCGAGCAAGTGGGAATATTCAAAATTTATTAGCATGGTATCAGCAGACACAGGAAAT	230		
250	GTCGAGCAAGTGGGAATATTCAAAATTTATTAGCATGGTATCAGCAGACACAGGAAAT	309		
231	CTCTCAGCTCTGCTGCTATTTCTGCAAAACCTTTAGCAGATGGTGGCATCAAGTTCA	290		
310	CTCTCAGCTCTGCTGCTATTAATCGAAAACCTTTAGCAGATGGTGGCATCAAGTTCA	369		
291	GTGCAGTGGATCAGGAACACAATTTCTCTCAAGATCAACAGCCTGAGCCTGAAGATT	350		
370	GTGCAGTGGATCAGGAACACAATTTCTCTCAAGATCAACAGCCTGAGCCTGAAGATT	429		
351	TTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCGTACAGTTTCGGGGGGGACCA	410		
430	TTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCGTACAGTTTCGGGGGGGACCA	489		
411	AGCTGAAATAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCACCACATCCAGTG	470		
490	AGCTGAAATAAACGGCTGATGCTGCACCAACTGTATCCATCTTCCACCACATCCAGTG	549		
471	AGCAGTTAATCTCGAGTGGCTCAGTGGTGGTCTTGAACAACTTCTACCCCAAAG	530		
550	AGCAGTTAATCTCGAGTGGCTCAGTGGTGGTCTTGAACAACTTCTACCCCAAAG	609		
531	ACATCAATGTCAAGTGGAGATTGTATGGCAGTGAAGCAGCAAAATGGCTCTGAACGTT	590		
610	ACATCAATGTCAAGTGGAGATTGTATGGCAGTGAAGCAGCAAAATGGCTCTGAACGTT	669		
591	GGACTGATCAGGACGCAAGACAGCACCCTACAGCATGAGCAGCACCCTCAATTGACCA	729		
670	GGACTGATCAGGACGCAAGACAGCACCCTACAGCATGAGCAGCACCCTCAATTGACCA	650		
651	AGGACGAGTATGAACGACATAACAGCTATACCTGTGGGCCACTTCACAAAGACATCACT	710		
730	AGGACGAGTATGAACGACATAACAGCTATACCTGTGGGCCACTTCACAAAGACATCACT	789		
711	CAGCCATTGTCAAGAGCTTCAACAGGAATGAGTGTATTAGACACAAG	756		
790	CAGCCATTGTCAAGAGCTTCAACAGGAATGAGTGTATTAGACACAAG	835		

RESULT 6
 3-08-792-824-1
 Sequence 1, Application US/08792824
 Patent No. 5932449

```

GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHVEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Chemical and Biological Defense
ADDRESSEE: Command
STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
STATE: MD
COUNTRY: U.S.
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792.824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4435 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: BALB/c
IMMEDIATE SOURCE:
CLONE: Clone pHist 5
US-08-792-824-1

Query Match
Best Local Similarity 63.9%; Score 626; DB 2; Length 4435;
Matches 656; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 51 TGCTCACTCAGGTCTCTCGGTTGCTGCTGCTGTACAGGTGCCAGATGTGACATCC 110
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2264 TGCCTACGGCGCGCTGGATTGTTATTACTCGCTGCCAACCGCATGGCGGACATCC 2323
QY 111 AGATGACTCAGTCTCCAGCTCCCTATCTCATCTGTGGGAGAACTGTCCACATCACAT 170
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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2384 GTCGACCAAGTGGGAATATTCAAATTAATTAGCATGGTATCAGCAGAAACAGGGAAT 2443
QY 231 CTCCTCAGCTCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGGCCATCAAGTTCA 290
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2444 CTCCTCAGCTCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGGCCATCAAGTTCA 2503
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2504 GTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCTGAAGATT 2563
QY 351 TTGGAGATTATTACTGTCAACATTTTGGAGTACTCCGTACACGTTCCGGAGGGGACCA 410
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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us-09-770-916-3.rni

Tue Jul 1 18:41:00 2003

2564 TTGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTGGAGCTGGGTGGAGGCCACCA 2623
 411 AGCTGGAAATAAAGGGGCTGATGCTGCACCACTGTATCCATCTCCACCATCCAGTG 470
 2624 AGCTGGAAATCAACGGGCTGATGCTGCACCACTGTATCCATCTCCACCATCCAGTG 2683
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 2684 AGCAGTTAAACATCTGGAGGTCCTGCTGCTTGAACAACTTCTACCCCAAG 2743
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 2744 ACATCAATGTCAAGTGGAGATGTGATGAGTGAACGACAAATGGCTCTGACACAGTT 2803
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 2804 GGACTGATCAGACAGCAAGACAGACACCTACAGCATGAGCAGCACCTCTACGTTGACCA 2863
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 711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAG 756
 2924 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAG 2969

RESULT 7

Sequence 8, Application US/08792824
 Patent No. 5932449
 GENERAL INFORMATION:
 APPLICANT: EMANUEL, PETER A.
 APPLICANT: BURANS, JAMES P.
 APPLICANT: VALDES, JAMES J.
 APPLICANT: MOHVEE, ELDEFRAWI E.
 TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: U.S. Army Chemical and Biological Defense
 ADDRESS: Office of the Chief Counsel, Bldg E4435
 STREET: Aberdeen Proving Ground
 CITY: Aberdeen Proving Ground
 STATE: MD
 COUNTRY: U.S.
 ZIP: 21010-5423

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08792,824
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Biffoni, U. J.
 REGISTRATION NUMBER: 39,908
 REFERENCE/DOCKET NUMBER: DAM 431-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 410-671-1158
 TELEFAX: 410-671-2534
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1632 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: cdna
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE: Mus musculus

STRAIN: BALB/C
 IMMEDIATE SOURCE:
 CLONE: PH1st 20
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 88..798
 OTHER INFORMATION: /product= "antibody fragment, light chain"
 OTHER INFORMATION: /label= BotFab 20
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 818..1582
 OTHER INFORMATION: /product= "antibody fragment, Heavy Chain"
 OTHER INFORMATION: /label= BotFab 20
 OTHER INFORMATION:
 US-08-792-824-8

Query Match 63.6%; Score 622.8; DB 2; Length 1632;
 Best Local Similarity 92.6%; Pred. No. 9e-141;
 Matches 654; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 QY 51 TGCTCACTCAGGTCCTGGGCTTCTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCC 110
 Db 101 TGGCTACGGCGCGCTGGATTCTTATTACTCGCTGCCCAACCCAGCATGGCCGACATCC 160
 QY 111 AGATGACTCAGTCTCCAGCCTCCCTATCTGCTATCTGCTGTGGAGAACTGTCCACATCAT 170
 Db 161 AGATGACCCAGTCTCCAGCCTCCCTATCTGCTATCTGCTGTGGAGAACTGTCCATCATCAT 220
 QY 171 GTGAGCAAGTGGGAATATTCAAAATTTATTAGCATGTATCAGCAGACACAGGAAAT 230
 Db 221 GTGAGCAAGTGGGAATATTCAAAATTTATTAGCATGTATCAGCAGACACAGGAAAT 280
 QY 231 CTCCTCAGTCTCTGCTTATCTGCAAAACCTTAGCAGATGTTGTCCTCAAGTTTCA 290
 Db 281 CTCCTCAGTCTCTGCTTATTAATGCAAAACCTTAGCAGATGTTGTCCTCAAGTTTCA 340
 QY 291 GTGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT 350
 Db 341 GTGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT 400
 QY 351 TTGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTGAGTACTCCGTGGAGGTCGAGGAGGCCACCA 410
 Db 401 TTGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTGAGTACTCCGTGGAGGTCGAGGAGGCCACCA 460
 QY 411 AGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCTTCCACCATCCAGTG 470
 Db 461 AGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCTTCCACCATCCAGTG 520
 QY 471 AGCAGTTAAACATCTGGAGTGGCTCAGTCTGCTGCTTGTGAACAACCTTCTACCCCAAG 530
 Db 521 AGCAGTTAAACATCTGGAGTGGCTCAGTCTGCTGCTTGTGAACAACCTTCTACCCCAAG 580
 QY* 531 ACATCAATGTCAAGTGGAAAGATTGATGGCAGTCAACAGCAAAATGGCTCTGCAACAGTT 590
 Db 581 ACATCAATGTCAAGTGGAAAGATTGATGGCAGTCAACAGCAAAATGGCTCTGCAACAGTT 640
 QY 591 GGACTGATCAGGACAGCAAGACAGCAGCCTTACAGCATGAGCAGCACCTCCCTGACCA 650
 Db 641 GGACTGATCAGGACAGCAAGACAGCAGCCTTACAGCATGAGCAGCACCTCCCTGACCA 700
 QY 651 AGGACGAGTATGACGACATTAACAGCTTATACCTGTGAGGCCACTTCAACAAGACATCACTT 710
 Db 701 AGGACGAGTATGACGACATTAACAGCTTATACCTGTGAGGCCACTTCAACAAGACATCACTT 760
 QY 711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAG 756
 Db 761 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAAG 806

RESULT 8
 US-08-303-569B-4
 ; Sequence 4, Application US/08303569B

Patent No. 5859205
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5859205rls
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569B
FILING DATE: 07-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yoko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 18..722
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 84..722
US-08-303-569B-4

Query Match 62.98; Score 615.6; DB 2; Length 943;
Best Local Similarity 84.68; Pred. No. 4.1e-139;
Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;
Y 96 CCAGATGTGACATCCAGATGACTCAGTCCAGCTCCCTATCTGTCATCTGTGGGAGAA 155
b 76 CCAGAGGACAAATTGTTCTCACCAGTCTCCAGCAATCATGTCTGTCATCTCCAGGGAGA 135
Y 156 CTGTACCATCATCATCGAGCAAGTGGGAATATTCAAAATTTATTTAGCATGTATCAGC 215
b 136 AGTCCACCATGACCTGCAGTGCAGCTCAGTGT---AGTTACATGAATGTGTACGAGC 192
Y 216 AGACAGAGGAAATCTCTAGCTCCTGCTTATCTGCAAAACCTTAGCAGATGGTG 275
b 193 AGAAGTCAGGACCTCCCAAAAGATGATTATGACACATCCAACTGGCTTGGAG 252
Y 276 TGCCATCAAGTTGACGTGATGATGAGGACACAAATTTCTTCAAGATCAACAGCC 335
b 253 TCCCTGCTCACTTCAAGGGCAGTGGGTCTGGGACCTTACTCTCTCAATCAGGGGCA 312
Y 336 TGACGCTGAAGATTTTGGAGTTTACTGTCAACATTTTGGAGTACTCGTACAGT 395
b 313 TGGAGGCTGAGATGCTGCACTTATTATGCGCAGTGGAGTAGTACCACTTCACT 372
Y 396 TCGAGGGGGGACCAAGCTGAAATATAAAGCGGCTGATGTCACCAACTGTATCCATCT 455
b 373 TCGGCTCGGGGACAAAGTTGAAATAAACCGGGGTGACTGACCAACTGTATCCATCT 432

QY 456 TCCACCATCCAGTGGAGGTTAAATCTGGAGGTGCCCTCAGTCGTGTCTTCTGAACA 515
Db 433 TCCACCATCCAGTGGAGGTTAAATCTGGAGGTGCCCTCAGTCGTGTCTTCTGAACA 492
QY 516 ACTTCTACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATG 575
Db 493 ACTTCTACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATG 552
QY 576 GCGTCTGAACAGTTGGAGTATGATGAGGACAGCAAGACAGACACCTACAGCATGAGCAGCA 635
Db 553 GCGTCTGAACAGTTGGAGTATGATGAGGACAGCAAGACAGACACCTACAGCATGAGCAGCA 612
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Db 613 CCCTCAGCTTGACCAAGGACGAGTATGATGAGGACAGCAAGACAGACACCTACAGCATGAGCAGCA 672
QY 696 ACAAGACATCAACTTCACCCATTTCAAGAGCTTCAACAGAGTGAAGTGAAGACAAA 755
Db 673 ACAAGACATCAACTTCACCCATTTCAAGAGCTTCAACAGAGTGAAGTGAAGACAAA 732
QY 756 GGTCTCTGAGAGCGCCACCAAGGACGCTCCAGCTCCATCTATCTTCCCTTCAAGGTCTTG 815
Db 733 GGTCTCTGAGAGCGCCACCAAGGACGCTCCAGCTCCATCTATCTTCCCTTCAAGGTCTTG 791
QY 816 GAGGCTTCCCAAGGACGCTACCACTTGGGTGCTCCAAACCTCTCCCTCCACCTCC 875
Db 792 GAGGCTTCCCAAGGACGCTACCACTTGGGTGCTCCAAACCTCTCCCTCCACCTCC 849
QY 876 TTCT 935
Db 850 TTCT 909
QY 936 TAAAGTGAGTCTTTGCAAAAAA 969
Db 910 TAAAGTGAGTCTTTGCAAAAAA 943

RESULT 9
US-08-116-247-4
Sequence 4, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212rls
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100

us-09-770-916-3.rni

Tue Jul 1 18:41:00 2003

TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 943 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 18..722
 -08-116-247-4

Query Match 62.9%; Score 615.6; DB 2; Length 943;
 Best Local Similarity 84.6%; Pred. No. 4.1e-139;
 Matches 739; Conservative 0; Mismatches 129; Indels 6; Gaps 4;
 96 CCAGATGTGACATCCAGTACTCAGTCTCCAGGCTCCCTATCTGCAATCTCTGGGAGAAA 155
 76 CCAGAGGACAAATGTTCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGA 135
 156 CTGTCACCATCACATGTGCGAAGTGGGAATATTCAAAATTTATTAGCATGGTATCAGC 215
 136 AGGTCACCATGACCTGCGAGTGGCAGCTCAAGTGT--AAGTTACATGAATGGTACCAGC 192
 216 AGACACAGGGAAATCTCCTCAGCTCCTGGTGTATCTGCAAAACCTTAGCAGATGGTG 275
 193 AGAAGTCAGGCACTCCCCCAAGATGATTTATGACACATCCAACTGGCTTCTGGAG 252
 276 TGCCATCAAGTTTCAGTGGCATGTGATCAGGACACAAATATTCTCAAGATCAACAGCC 335
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 336 TGCAGCTCAAGATTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACACGT 395
 313 TGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCTGGAGTAGTAAACCCATTACGT 372
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 373 TCGGCTCGGGGACAAAGTTGGAAATTAACCGGGCTGATCTGACCACTGTATTCATCT 432
 456 TCCACACATCCAGTGCAGTAACTATCTGAGAGTGGCTCAGTCGTGCTTCTGAACA 515
 433 TCCACCATCCAGTGCAGTAACTATCTGAGAGTGGCTCAGTCGTGCTTCTGAACA 492
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 493 ACTTCTACCCCAAGACATCAATGTCAGTGAAGATTGATGGCAGTGAACGACAAATG 552
 576 GCGTCTGACAGTGGATGATCAGGACGCAAGACAGCAGCCTACAGCATGAGCAGCA 635
 553 GCGTCTGACAGTGGATGATCAGGACGCAAGACAGCAGCCTACAGCATGAGCAGCA 612
 636 CCCTCAGCTTACCAAGGACGAGTATGAACGACATACAGCTATACCTGTGAGGCACTC 695
 613 CCCTCAGCTTACCAAGGACGAGTATGAACGACATACAGCTATACCTGTGAGGCACTC 672
 696 ACAAGACATCAACTTACCCCTTTGCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA 755
 673 ACAAGACATCAACTTACCCCTTTGCAAGAGCTTCAACAGGAATGAGTGTAGAGACAAA 732
 756 GGTCTGAGAGCCACACAGCTCCAGCTCCAGTCCATCTTCTCCCTTCTAAGTCTTTG 815
 733 GGTCTGAGAGCCACACAGCTCCAGCTCCAGTCCATCTTCTCCCTTCTAAGTCTTTG 791
 816 GAGGCTTCCCAACAGGACCTTACCACTCTGCGGTGCTCCAAACCTCTCCCCACCTCC 875
 792 GAGGCTTCCCAACAGGACCTTACCACTCTGCGGTGCTCTAAACCTCT-CCCACCTCC 849
 876 TTCT 935
 850 TTCT 909
 936 TAAAGTGAAGTCTTTTGGCAAAAAA 969

Db 910 TAAAGTGAAGTCTTTGGCTTGAAAAA 943
 RESULT 10
 US-08-792-824-5
 ; Sequence 5, Application US/08792824
 ; Patent No. 5932449
 ; GENERAL INFORMATION:
 ; APPLICANT: EMANUEL, PETER A.
 ; APPLICANT: BURANS, JAMES P.
 ; APPLICANT: VALDES, JAMES J.
 ; APPLICANT: MOHYEE, ELDEFRAWI E.
 ; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: U.S. Army Chemical and Biological Defense
 ; ADDRESSEE: Command
 ; STREET: Office of the Chief Counsel, Bldg E4435
 ; CITY: Aberdeen Proving Ground
 ; STATE: MD
 ; COUNTRY: U.S.
 ; ZIP: 21010-5423
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/792,824
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Biffoni, U. J.
 ; REGISTRATION NUMBER: 39,908
 ; REFERENCE/DOCKET NUMBER: DAM 431-96
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 410-671-1158
 ; TELEFAX: 410-671-2534
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1641 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; STRAIN: BALB/c
 ; IMMEDIATE SOURCE:
 ; CLONE: phist 1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 87..788 /product= "antibody fragment, light
 ; OTHER INFORMATION: "chain"
 ; OTHER INFORMATION: /label= BotFab 1
 ; NAME/KEY: CDS
 ; LOCATION: 815..1579 /product= "antibody fragment, Heavy
 ; OTHER INFORMATION: "chain"
 ; OTHER INFORMATION: /label= BotFab 1
 ; US-08-792-824-5

Query Match 61.0%; Score 597.2; DB 2; Length 1641;
 Best Local Similarity 92.2%; Pred. No. 1.3e-134;
 Matches 651; Conservative 0; Mismatches 53; Indels 2; Gaps 2;
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 936 TAAAGTGAAGTCTTTTGGCAAAAAA 969

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QY	111	AGATGACTAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCAACCATCATC	170
Db	160	AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCACTATCATC	219
QY	171	GTGAGCAAGTGGGAATATTCAAAATATTATTAGCATGTATCAGCAGACAGGAAAT	230
Db	220	GTGAGCAAGTGGGAATATTCAAAATATTATTAGCATGTATCAGCAGAAACAGGAAAT	279
QY	231	CTCCTCAGTCTCTGGTCTATTCTGCAAAACCTTAGCAGATGTTGTGCCATCAAGTTCA	290
Db	280	CTCCTCAGTCTCTGGTCTATAATGCAAAAACCTTAGCAGATGTTGTGCCATCAAGTTCA	339
QY	291	GTGGCAGTGGATCAGNACACAAATATCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT	350
Db	340	GTGGCAGTGGATCAGNACACAAATATCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT	399
QY	351	TTGGGAGTTATTACTGTCTCAACATTTTGGAGTACTCCGTACAGTTCGAGGGGGACCA	410
Db	400	TTGGGAGTTATTACTGTCTCAACATTTTGGAGTACTCCGTGAGCGTTCGGTGGAGGCACCA	459
QY	411	AGCTTGGAAATAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTG	470
Db	460	AGCTTGGAAATAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTG	519
QY	471	AGCAGTTAAACATCTGGAGTGCGTCAAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAG	530
Db	520	AGCAGTTAAACATCTGGAGTGCGTCAAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAG	579
QY	531	ACATCAATGTCAAGTGAAGATTGATGCGACTGAAACAAATATGGCGCTGAACAGTT	590
Db	580	ACATCAATGTCAAGTGAAGATTGATGCGACTGAAACAAATATGGCGCTGAACAGTT	639
QY	591	GGACTGATCAGGACAGAAAGACAGCACTACAGCATGAGCAGCAGCCTCAGTGTGACCA	650
Db	640	GGACTGATCAGGACAGAAAGACAGCACTACAGCATGAGCAGCAGCCTCAGTGTGACCA	699
QY	651	AGGACGAGTATGACACATCAACAGCTATACCTGTGAGGCCACTCACAAGACATCACTT	710
Db	700	AGGACGAGTATGACACATCAACAGCTATACCTGTGAGGCCACTCACAAGACATCACTT	759
QY	711	CACCATTTCTCAAGAGCTTCAACAGGAATGAGTGTAGACACAAAG	756
Db	760	C-CCCATTTCTAGAGCTTC-CCAGGAATGAGTGTATAGCAAGG	803

RESULT 11

3-08-7834-783A-2
 Sequence 2, Application US/08634783A
 Patent No. 5861276
 GENERAL INFORMATION:
 APPLICANT: KWAK, JU-WON
 APPLICANT: HAN, MOON-HI
 APPLICANT: CHOI, BYUNG-KWON
 TITLE OF INVENTION: C-DNAS ENCODING MURINE ANTIBODY
 TITLE OF INVENTION: AGAINST HUMAN PLASMA APOLIPOPROTEIN B-100
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DILWORTH & BARRESE
 STREET: 333 EARLE OVINGTON BLVD.
 CITY: UNIONDALE
 STATE: NY
 COUNTRY: USA
 ZIP: 11553
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/634,783A
 FILING DATE: 19-APR-1996

```

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BARRESE, ROCCO S.
REGISTRATION NUMBER: 25,253
REFERENCE/DOCKET NUMBER: 685-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFAX: 516-228-8516
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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Query Match	52.8%;	Score 517.2;	DB 2;	Length 642;
Best Local Similarity	87.9%;	Pred. No. 1.6e-115;		
Matches 564;	Conservative 0;	Mismatches 78;	Indels 0;	Gaps 0;
104	GACATCCAGATCACTCAGTCTCCAGCCTCCCTATCTGCATCTCTGGGAGAAACTGTGCACC	163		
1	GATATCAAGATGACCCAGTCTCCATCTTCCATGTATGCATCTCTAGAGAGAGAGTCACT	60		
164	ATCACATGTCGACGAAGTGGGAATATTCAAAATATTATTAGCATGGTATCAGCAGACACAG	223		
61	ATCACTTCCAGGCCAGTCAGACACTATTATAGCTATTTAAAGCTGTTCACAGAGAACC	120		
224	GGAAATCTCCTCAGCTCTCGTCTATTCTTGCAAAACCTTTAGCAGATGGTGTGCCATCA	283		
121	GGGAAATCTCTAGACCCCTGATCTATCTGCGAAACAGATTGGTGTGATGGGTGCCATCA	180		
284	AGGTTCACTGGCAGTGGATCAGGACACAAATATTCTCTCAAGATCAACAGCCTGCAGCT	343		
181	AGGTTCACTGGCAGTGGATCAGGACAAATATTCTCTCAAGATCAACAGCCTGCAGCT	240		
344	GAAGATTTTGGGAGTTATTACTGTCACATTTTGGAGTACTCCGTACACGTTTCGGAGG	403		
241	GAAGATCTGGAAATTTATTATTGTTTACAGTTTGTATGAGTTTTCGGTACACGTTTCGGAGG	300		
404	GGACACAGCTGGAAATPAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA	463		
301	GGACACAGCTGGAAATPAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA	360		
464	TCACAGTGCAGCTTAACATCTGGAGTGCCTCAGTCTGTCTTCTTGAACAACTTCTAC	523		
361	TCACAGTGCAGCTTAACATCTGGAGTGCCTCAGTCTGTCTTCTTGAACAACTTCTAC	420		
524	CCCAAGACATCAATGCTCAAGTGGAGATTTGATGGAGTGAACGACAAAATGGCGTCTG	583		
421	CCCAAGACATCAATGCTCAAGTGGAGATTTGATGGAGTGAACGACAAAATGGCGTCTG	480		
584	ACAGTTGGACTGATCAGGACAGAAAGACAGCACCTACAGCATGAGCAGACCCCTACG	643		
481	ACAGTTGGACTGATCAGGACAGAAAGACAGCACCTACAGCATGAGCAGACCCCTACG	540		
644	TTGACCAAGGACGAGTATGACGACATACAGCTATACCTGTGAGGCCACTTCAAGACA	703		
541	TTGACCAAGGACGAGTATGACGACATACAGCTATACCTGTGAGGCCACTTCAAGACA	600		
704	TCAACTTCAACCATTTCAAGAGCTTCAACGGAATGAGTGT	745		
601	TCAACTTCAACCATTTCAAGAGCTTCAACGGAATGAGTGT	642		

RESULT 12

US-97-070-817-2
; Sequence 2, Application US/03070817
; Patent No. 6096516
; GENERAL INFORMATION:
; APPLICANT: KWAK, JU-WON
; APPLICANT: HAN, MOON-HI

Db ₁	421	CCCAAAGACATCAATGTCAACTGGAAGATTGATGGCAGTTGAACGACAAAATGGCGTCTG	480
QY	584	AACAGTTGGACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCCCTCAG	643
Db	481	AACATTTGGACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCCCTCAG	540
QY	644	TTGACCAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCGCACTCACAGACA	703
Db	541	TTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCGCACTCACAGACA	600
QY	704	TCAACTTCACCCATTTGTCAGAGCTTCAACAGGAATGAGTGT	745
Db	601	TCAACTTCACCCATTTGTCAGAGCTTCAACAGGAATGAGTGT	642

RESULT 13

RESOLUTION 737-129A-7
US-08-737-129A-7
Sequence 7, Application US/08737129A
Patent No. 5885816
GENERAL INFORMATION:
APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,129A
FILING DATE: NO. 5885816member 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-737-129A-7

	Query Match	52.1%;	Score 509.6;	DB 2;	Length 652;
	Best Local Similarity	87.0%;	Pred. No. 1.1e-113;		
	Matches 560;	Conservative	0;	Mismatches 84;	Indels 0;
					Gaps 0;
104	GACATCCAGATGCTCAGTCTCCAGCTCCCTATCTGCACTCTGGGAGAACTGTCAAC	163			
	1 GAGCTCGTATGATGCCAGACTCCATCTTCCATGTATGCATCTCTAGGAGAGAGTCACT	60			
Db					
164	ATCACATGTCGACGAAGTGGGAATATTCAAAATTTATAGCATGGTATCAGCAGACACAG	223			
QY					
61	ATCACTTGCAGGCGAGCTCAGGACATTAATATCTATTTAAGTTGGTCTCCAGCAGAAACCA	120			
Db					
224	GGAAATCTCCTCAGCTCCCTGGTCTATTTCTGCAAAAACCTTTAGCAGATGGTGTGCCATCA	283			
QY					

Query Match	52.8%	Score 517.2	DB 3	Length 642
Best Local Similarity	87.9%	Pred. No. 1.6e-115		
Matches 564	Conservative 0	Mismatches 78	Indels 0	Gaps 0
104	Y	GACATCCAGATGACTCAGTCTCCACGCCCTCCCTATCTGCATCTGTGGAGAACTGTCCACC	163	
	Y			
	Y			
	Y			
1	b	GATATCAAGATGACCCAGTCTCCATCTTCCATGTATGCATCTCTAGGAGAGAGATCACT	60	
	Y			
164	Y	ATCACATGTGCGAGCAAGTGGGAATATTCAAATTTATTAGCATGTATCACACACACAG	223	
	Y			
61	b	ATCATTTGCAAGCGAGTCAGGACATTTATAGCTATTTAAAGCTGGTTCACAGCAAAACCA	120	
	Y			
224	Y	GGAAATCTCCTCAGTCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGCCATCA	283	
	Y			
	Y			
121	b	GGAAATCTCCTTAAGACCCCTGATCTATCTGTCGCAACAGATTGGTGCATGGGTGCCATCA	180	
	Y			
284	Y	AGTTTCAGTGGCAGTGGATCAGGAACACAAATATTCTCTCAAGATCAACAGCCTGCAGCCT	343	
	Y			
181	b	AGTTCAGTGGCAGTGGATCTGGCAAGATTATTCTCTCACCATCAGCAGCCTGGAGTAT	240	
	Y			
344	Y	GAAGATTTTGGGATTTATTACTCTCAACATTTTGGAGTACTCCGTACACGTTCCGAGGG	403	
	Y			
241	b	GAGATCTGGGAATTTATTATTCTACAGTTTGTATGAGTTTCCGTACACGTTCCGAGGG	300	
	Y			
404	Y	GGGACCAAGCTGGAAATAAACGGGCTGATGCTGCACCACTGTATCCCATCTTCCACCA	463	
	Y			
301	b	GGGACCAAGCTGGAAATAAACGGGCTGATGCTGCACCACTGTATCCCATCTTCCACCA	360	
	Y			
464	Y	TCCAGTGAGCAGTTAAACATCTGGAGGTCCTCAGTCTGTGCTTCTTGAACAACTTCTAC	523	
	Y			
361	b	TCCAGTGAGCAGTTAAACATCTGGAGGTCCTCAGTCTGTGCTTCTTGAACAACTTCTAC	420	
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524	..	CTCAAGACATCAATGTCTCAAGTGGGAAGATTGATGGCAGTGAACGACAAATGCGCTCTTG	583	
	..			

Db 121 GGAATCTCTTAAGGCCCTGATCTATCTGATACAAAGGATTTGGTAGATGGGTCCCATCA 180
QY 284 AGGTTAGTGGCAGTGGATCAGGAGACACAAATATCTCTCAAGATCAACAGCCTGAGCCT 343
Db 181 AGGTTAGTGGCAGTGGATCAGGAGACACAAATATCTCTCAAGATCAACAGCCTGAGCCT 246
QY 344 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGGTTCGAGGG 403
Db 241 GAAGATATGGGAAATTTATTTATTTGCTACAGTATGATGATTTCCGTACAGGTTCGAGGG 300
QY 404 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 463
Db 301 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 360
QY 464 TCCAGTGGAGCATTTAAACATCTGGAGTGCCTCAGTCGTGCTTCTTGAACAACTTCTAC 523
Db 361 TCCAGTGGAGCATTTAAACATCTGGAGTGCCTCAGTCGTGCTTCTTGAACAACTTCTAC 420
QY 524 CCCAAAGACATCAATGTCAAGTGAAGATTGATGCGAGTGAACGACAAATGGGCTCTG 583
Db 421 CCCAAAGACATCAATGTCAAGTGAAGATTGATGCGAGTGAACGACAAATGGGCTCTG 480
QY 584 AACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCTATACCTGTGAGGCCACTCACAAGACA 703
Db 481 AACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCTATACCTGTGAGGCCACTCACAAGACA 600
QY 644 TTGACCAAGACAGCATGATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACA 703
Db 541 TTGACCAAGACAGCATGATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAGACA 600
QY 704 TCAACTTCAACCATTTCTCAAGAGCTTCAACAGCAATGAGTGTTA 747
Db 601 TCAACTTCAACCATTTCTCAAGAGCTTCAACAGCAATGAGTGTTA 644

RESULT 14 5453363-1
; Patent No. 5453363
; APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF
; TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR
; AFTER GENETIC EXPRESSION IN PROKARYOTES
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,044
; FILING DATE: 02-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 942,370
; FILING DATE: 09-SEP-1992
; APPLICATION NUMBER: 498,500
; FILING DATE: 23-MAR-1990
; APPLICATION NUMBER: 76,207
; FILING DATE: 23-OCT-1986
SEQ ID NO: 1:
LENGTH: 5238
453363-1

Query Match 49.68; Score 485.8; DB 6; Length 5238;
Best Local Similarity 82.68; Pred. No. 1e-107;
Matches 556; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Y 104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGATCTGTGGAGAACTGTCCACC 163
b 7 GATATTGTCTAATCTAGTCTCCAGCCACCTGTGTGACTCCAGAGATAGCGTCACT 66
Y 164 ATCACAATGTCGAGCAAGTGGGAATATTTCAAAATTTATTTAGCATGGTATCAGCAGACAG 223
b 67 CTCTCTGCGAGCCGACCAAGATTTAGCAACAACCTACAGTGGTATCAACAAAATCA 126
Y 224 GGAATATCTCCTCAGTCTCTGCTTATTTGCAAAAACCTTTAGCATGGTGTGCCATCA 283
b 127 CATGAGTCTCCAAGGCTTCTCATCAATATGCTTCCAGATCCATCTCTGGATCCCTCT 186

QY 284 AGTTCAGTGGCAGTGGATCAGGAGACACAAATATCTCTCAAGATCAACAGCCTGAGCCT 343
Db 187 AGTTCAGTGGCAGTGGATCAGGAGACACAAATATCTCTCAAGATCAACAGCCTGAGCCT 246
QY 344 GAAGATTTGGGAGTTATTTACTGTCAACATTTTGGAGTACTCCGTACAGGTTCGAGGG 403
Db 247 GAAGATTTGGGAAATTTATTTGCTACAGATTAACAGCTGGCCTCTCAGGTTCGCTGCT 306
QY 404 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 463
Db 307 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGCACCAACTGTATCCATCTTCCACCA 366
QY 464 TCCAGTGGAGCATTTAAACATCTGGAGTGCCTCAGTCGTGCTTCTTGAACAACTTCTAC 523
Db 367 TCCAGTGGAGCATTTAAACATCTGGAGTGCCTCAGTCGTGCTTCTTGAACAACTTCTAC 426
QY 524 CCCAAAGACATCAATGTCAAGTGAAGATTGATGCGAGTGAACGACAAATGGGCTCTG 583
Db 427 CCCAAAGACATCAATGTCAAGTGAAGATTGATGCGAGTGAACGACAAATGGGCTCTG 486
QY 584 AACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCTATACCTGTGAGGCCACTCACAAGACA 703
Db 487 AACAGTTGGACTGATCAGGACAGCAAGACAGCACTACAGCTATACCTGTGAGGCCACTCACAAGACA 606
QY 704 TCAACTTCAACCATTTCTCAAGAGCTTCAACAGCAATGAGTGTTAGAGACAAAGTCTCTGA 763
Db 607 TCAACTTCAACCATTTCTCAAGAGCTTCAACAGCAATGAGTGTTAGAGACAAAGTCTCTGA 666
QY 764 GACGCCACCAACCA 776
Db 667 GACGCCACCAACCA 679

RESULT 15 US-09-170-769A-7
; Sequence 7, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT
; FILE REFERENCE: SCRIPI1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(633)
; OTHER INFORMATION: CDR1-Nucleic acids 61-93; CDR2-Nucleic acids 139-159; CDR3-Nuc
; OTHER INFORMATION: c acids 256-28
US-09-170-769A-7

Query Match 49.34; Score 482.6; DB 4; Length 633;
Best Local Similarity 85.28; Pred. No. 3.2e-107;
Matches 539; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 113 ATGACTCAGTCTCCAGCCTCCCTATCTGATCTGTGGGAGAACTGTGACCATGT 172
Db 1 ATGACCCAGACTCCATCTCCCTCTCTGCTCTCTGAGGACAGAGTCCCATGTGC 60

us-09-770-916-3.rni

Tue Jul 1 18:41:00 2003

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 653 GACGAGTATGAACGACATTAACGCTATACCTGTGAGCCACTCACAAAGACATCAACTTCA 712
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 713 CCCATTGTCAAGAGCTTCACAGGAATGAGTGT 745
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Search completed: June 24, 2003, 01:22:35
 Job time : 55.8675 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:23:42 ; Search time 245.227 Seconds
(without alignments)
8990.482 Million cell updates/sec

Title: US-09-770-916-3
Perfect score: 979
Sequence: 1 accaccttctgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	ID	Description
1	708.6	72.4	751	16	AAT51437
2	693.4	70.8	1041	15	Murine MAB SK48-E2
3	693.4	70.8	1041	15	T84.12 light chain
4	677	69.2	882	5	AAQ54653
5	673.8	68.8	882	5	T84.12 L4-12-1 lig
6	667.6	68.2	927	20	CDNA insert of pK1
7	652	66.6	961	16	mrna encoding kapp
8	650.6	66.5	952	16	Anti-p21(ras) mono
9	634.2	64.8	5711	24	Anti-tobacco mosai
					MAB 55.1 light cha
					Alpha-lactalbumin

10	634.2	64.8	6255	24	AAD28276	LNBDTDC vector #1.
11	634.2	64.8	6255	24	AAD28315	LNBDTDC vector #1.
12	634.2	64.8	7170	24	AAD28272	LSRNL vector. Chi
13	626	63.9	1644	20	AX86667	Murine anti-botuli
14	626	63.9	1672	20	AX86664	Murine anti-botuli
15	626	63.9	4435	20	AX86663	Murine anti-botuli
16	622.8	63.6	1632	20	AX86666	Murine anti-botuli
17	615.6	62.9	943	12	AX86666	Monoclonal antibod
18	598	61.1	882	14	AAQ12636	Monoclonal antibod
19	597.2	61.0	1641	20	AX86665	Murine anti-botuli
20	535	54.6	831	24	AAD29309	Human penton base
21	517.2	52.8	642	18	AAT85091	Mouse monoclonal a
22	509.6	52.1	652	17	AAT87818	Antibody 3G2 light
23	485.8	49.6	5238	11	AAQ04654	Plasmid pBT11 enc
24	483.2	49.4	724	20	AX90423	Chimeric antibody
25	476	48.6	1106	24	ABQ54241	Human ovarian anti
26	464.2	47.4	645	21	ABK13286	Mouse agglutinin
27	461.4	47.0	705	24	AX97063	DNA encoding TRA-8
28	460.2	47.1	1066	14	AAQ9943	Human anti-HBs lig
29	459.2	46.9	714	20	AX61085	Mouse immunoglobul
30	459	46.9	944	22	AAF4892	Human breast cance
31	458.8	46.9	723	16	AAQ92503	Mouse antibody F4-
32	455.4	46.5	627	16	AAQ0294	Monoclonal antibod
33	453.8	46.4	678	21	AAA27849	WOW-1 Fab light ch
34	453.2	46.3	974	24	AX99473	Anti-human AILIM m
35	452.2	46.2	639	10	AX91657	Chimeric antibody
36	452	46.2	738	21	AAZ61037	Nucleotide sequenc
37	450.4	46.0	1735	22	AAH47858	Mouse 6D9 catalyti
38	449.4	45.9	732	17	AAH42508	Murine A5B57 Light
39	449.4	45.9	732	20	AAV72081	Plasmid pEE14/A5B7
40	447.8	45.7	717	18	AAT88870	L chain subunit of
41	447.8	45.7	717	19	AAV66736	Anti-human Fas mon
42	447.8	45.7	717	21	AAH78203	Anti-human Fas ant
43	447.8	45.7	1526	13	AAQ21097	FabD1.3 in pUC19.
44	446.6	45.6	714	19	AAV70130	Anti-Fas MAB HFE7A
45	446.6	45.6	714	21	AAA72109	CDNA encoding mous

ALIGNMENTS

RESULT 1	
AAT51437	
ID	AAT51437 standard; DNA; 751 BP.
XX	
AC	AAT51437;
XX	
DT	24-JUN-1997 (first entry)
DE	Murine MAB SK48-E26 light chain DNA.
XX	
KW	Interleukin-1 beta; IL-1 beta; recombinant antibody;
KW	humanised antibody; chimeric antibody; antibody engineering;
KW	monoclonal antibody; MAB; SK48-E26; inflammation; therapy; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..14
FT	/*tag= a
FT	/note= "cloning adaptor"
FT	15..32
FT	/*tag= b
FT	33..737
FT	/*tag= c
FT	/product= SK48-E26 light chain
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FT	738..751
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FT	/note= "cloning adaptor"

RESULT 3
AAQ54653
AAQ5
AAQ5
24-J

[illegible]

406 TTGGAATAAAGCGGCTGATGTCACCAACTGTATCCATCTTCCACCATCCAGTGAG 465
473 CAGTTACATCTGGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAGAC 532
466 CAGTTAACTCTGGAGTGCCTCAGTCGTGTCTTGAACAACTTCTACCCCAAGAC 525
533 ATCAATCTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGCGTCTTGAACAGTTGG 592
526 ATCAATCTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGCGTCTTGAACAGTTGG 585
593 ACTGATCAGGACAGCAAGACAGACACCTTACAGCATGAGCAGCACCCTCAGCTTGACCAAG 652
586 ACTGATCAGGACAGCAAGACAGCACCCTTACAGCATGAGCAGCACCCTCAGCTTGACCAAG 645
653 GACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAACACATCAACTTCA 712
646 GACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAACGACATCAACTTCA 705
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773 ACCAGCTCCCAGCTCCATCTATCTTCCCTTCTAAGTCTTGGAGGCTTCCCCACAAGC 832
766 ACCAGCTCCCAGCTCCATCTATCTTCCCTTCTAAGTCTTGGAGGCTTCCCCACAAGC 825
833 GACCTACCACTCTTGGGCTGCTCCAAACCTCTCCCTCCCTCTCTCTCTCTCTCTCTCT 892
826 GACCTACCACTCTTGGGCTGCTCCAAACCTCTCCCTCCCTCTCTCTCTCTCTCTCTCT 885
893 TTCTTGGCTTTTATCATGCTAATATTTGCAGAAATATTCATTAAGTGAAGTCTTTGCA 952
886 TTCTTGGCTTTTATCATGCTAATATTTGCAGAAATATTCATTAAGTGAAGTCTTTGCA 945
953 AAAAAAAAAAAAAAAAAAAAAA 979
946 CTTGAAAAAAAAAAAAAAAAAAAA 972

RESULT 4
AN40022
AA40022 standard; cDNA; 882 BP.
AN40022;
01-DEC-1991 (first entry)
cDNA insert of pK17G4 encoding kappa anti-carcinoembryonic antigen.
Immunoglobulin; ds DNA; carcinoembryonic antigen; vector pK17G4.
EPI25023-A.
14-NOV-1984.
06-APR-1984; 84EP-0302368.
08-APR-1983; 83US-0483457.
(CITY) CITY OF HOPE.
(GETH) GENENTECH INC.
Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;
WPI; 1984-283749/46.
Immunoglobulin(s) produced by recombinant host cells - useful as
antibodies analogous to forms from mammals.
Disclosure; Fig. 2A-B; 79pp; English.
The cDNA is contained within recombinant vector pK17G4 and encodes
kappa anti-carcinoembryonic antigen chain. Using the vector the

CC immunoglobulin is produced readily in pure monoclonal form. Genetic
CC manipulations can be used to produce chimeras of variants drawing
CC their homology from species differing from each other. Protein
CC manipulation is also possible.
XX
SQ Sequence 882 BP; 231 A; 243 C; 194 G; 214 T; 0 other;
Query Match 69.2%; Score 677; DB 5; Length 882;
Best Local Similarity 85.7%; Pred. No. 1.9e-128;
Matches 752; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 76 GCTGCTGTGGCTTACAGTGCAGATGTGACATCCAGATGACTCAGTCTCCAGCTCCCT 135
DB 1 GTTCTGTGGTGTGCTGTGTTGAAGAGAGATTTGTGATGACCCAGCTCAAAATTCAT 60
QY 136 ATCTGATCTGTGGGAGAACTGTCCATCAGATGTGCGCAAGCTGGGAATATTTCAAAA 195
DB 61 GTCCACATCAGTAGGAGACAGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGGTGC 120
QY 196 TTATTTAGATGGTATCAGCAGACAGGAAATCTCTCAGCTCCCTGCTTATTTCTGC 255
DB 121 TGCTATAGCTGTATCAACAGAAACAGGACATCTCTTAACACTACTGATTTACTGGSC 180
QY 256 AAAAACTTAGCAGATGTGTCATCAAGTTCAGTGGCAGTGGATCAGGAACAATA 315
DB 181 ATCCACCCGGCACACTGGAGTCCCTGATCGCTCACAGGCGTGGGACAGATT 240
QY 316 TTCTCTCAAGATCAACAGCTGCAGCTGAAAGATTTGGAGTATTTAGTCTCAACATT 375
DB 241 CACTCTCACCATTGAATGTGAGTCTGATGCTTGGCAGATTTATTTGTCAACAATA 300
QY 376 TTGGAGTACTCCGTACACGTTGGAGGGGGGACCAAGCTGGAAATAAAGGGCTGATGC 435
DB 301 TAGCGGTATCTCTCCTCCTGCTGGAGCTGGAGCTGGAGCTGAAACGGCTGATGC 360
QY 436 TGCACCACTGTATCCATCTTCCACCATCTCAGTGGAGCTTAACATCTGGAGTGCCTC 495
DB 361 TGCACCACTGTATCCATCTTCCACCATCTCAGTGGAGCTTAACATCTGGAGTGCCTC 420
QY 496 AGTCGTGTCTTCTTGAACAACTTCTACCCAAAGACATCAATGTCAAGTGGAGATTGA 555
DB 421 AGTCGTGTCTTCTTGAACAACTTCTACCCAAAGACATCAATGTCAAGTGGAGATTGA 480
QY 556 TGGCAGTGAACGACAAATGGCGTCTGACAGTGGAGCTGATCAGCAGCAAGACAG 615
DB 481 TGGCAGTGAACGACAAATGGCGTCTGACAGTGGAGCTGATCAGCAGCAAGACAG 540
QY 616 CACCTACAGATGAGCAGCACCCTCAGCTTACCAAGGAGTATGAACACATAACAG 675
DB 541 CACCTACAGATGAGCAGCACCCTCAGCTTACCAAGGAGTATGAACACATAACAG 600
QY 676 CTATACCTGTGAGGCCACTCACAAGACATCAATTTCAAGTGGCTTTCAACAG 735
DB 601 CTATACCTGTGAGGCCACTCACAAGACATCAATTTCAAGTGGCTTTCAACAG 660
QY 736 GAATGAGTGTAGAGACAAAGTCTGAGAGCCACCAAGACCTCCAGCTCCCATCTCA 795
DB 661 GAATGAGTGTAGAGACAAAGTCTGAGAGCCACCAAGACCTCCAGCTCCCATCTCA 720
QY 796 TCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAAGGAGTATGAGTGGCTGCTC 855
DB 721 TCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAAGGAGTATGAGTGGCTGCTC 780
QY 856 CAAACCTCTCCCAAGCT 915
DB 781 CAAACCT 840
916 TATTTGCAGAAATATTTCAATAAAGTGGATCTTGA 952
841 TATTTGCAGAAATATTTCAATAAAGTGGATCTTGA 877

AAAN40023	
ID	AAAN40023 standard; mRNA; 882 BP.
XX	
AC	AAAN40023;
XX	
XX	01-DEC-1991 (first entry)
DE	mRNA encoding kappa anti-carcinoembryonic antigen.
DE	Immunoglobulin; ss mRNA; carcinoembryonic antigen.
KW	
XX	
FH	Key
FT	Location/Qualifiers
FT	1..673
XX	/*tag= a
PN	EP125023-A.
XX	
XX	14-NOV-1984.
XX	
PF	06-APR-1984; 84EP-0302368.
XX	
XX	08-APR-1983; 83US-0483457.
PR	(CITY) CITY OF HOPE.
PPA	(GETH) GENENTECH INC.
XX	
XX	Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD;
PPI	
XX	WPI; 1984-283749/46.
DR	P-PSDB; AAP40031.
DR	
XX	
PT	Immunoglobulin(s) produced by recombinant host cells - useful as
PT	antibodies analogous to forms from mammals.
XX	
XX	Disclosure; Fig. 3; 79pp; English.
XX	
CC	The mRNA is the coding sequence of the cDNA fragment contained within
CC	recombinant vector pK17G4 (see AAAN40022). It encodes kappa anti-
CC	carcinoembryonic antigen chain. Using the vector the immunoglobulin is
CC	produced readily in pure monoclonal form. Genetic manipulations can be
CC	used to produce chimeras of variants drawing their homology from species
CC	differing from each other. Protein manipulation is also possible.
XX	
XX	Sequence 882 BP; 231 A; 244 C; 194 G; 213 U; 0 other;
IQ	

```

Query Match      68.8%; Score 673.8; DB 5; Length 882;
Best Local Similarity 64.5%; Pred. No. 8.3e-128;
Matches 566; Conservative 184; Mismatches 127; Indels 0; Gaps 0;

y Y 76 GGTGCTGTGGCTTACAGATGCCAGATGTGCATATCCAGATCAGTCTCCAGCTCCCT 135
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 1 GUUGCUGUGUUCUGUGUGUUAAGAGGACAUUGUGAUGACCCAGUCUCAAAUUCAU 60

y Y 136 ATCTGCATCTGTGGGAGAACTGTCCACATCACATGTCGACAAAGTGGGAATATCAAA 195
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 61 GUCCACAUCAGUAGGAGACAGGUCAGCAUACCUGCAAGGCCACGAGGUGGGUGGC 120

y Y 196 TTATTTAGCATGTTATCAGCAGACACAGGGAAAATCTCTCAGTCTCTGTGTTATTCTGC 255
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 121 UCUUAUGCCUGGUUAUACAAGAACACGAGCAAUCCUUAACUACUGAUUUACUGGGC 180

y Y 256 AAAAACCTTAGCAGATGTGTGCCATCAAGTTTCAGTGGCAGTGGATCAGGAACAACAAT 315
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 181 AUCCACCCGGCACUGGAGUCCUCUGAUCCUUCACGAGUGAUCUGGGACAGAUUU 240

y Y 316 TTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTT 375
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 241 CACUUCACCAUUAUGAUGUGCUGAUGACUUGGCAGAUUUAUUCUGUCAACAUAU 300

y Y 376 TTGGAGTACTCCGTACAGTTCGAGGGGGGACCAAGCTCGAAATAAAGCGGCTGATGC 435
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b 301 UAGCGGUUAUCCUUCACAGUUCUGGUGCGGACCAAGCAGCUGAAACGGGCUAUG 360

```

[illegible]

QY	154	ATCATCATCTCGACGAAGTGGGAATATTC-----AAAATATTTAGCATGG	208
Db	154	ATCTCCTCGAGTCTAGTAAAGAGTCTCTGCATAGTAATGGCAACGCTTTCTTGTATTGG	213
QY	209	TATCAGCAGACAGAGGGAANAATCTCTCAGCTCCTCTGATTTCTGCAAAAACCTTTAGCA	268
Db	214	TTCTACAGAGGCTAGGCCAGTCTCTCAGCTCCTGATATATCGGATATCCAAACCTTGCC	273
QY	269	GATGGTGTGCCATCAAGSTTCAGTGGCAGTGGATCAGGAACACAATATTTCTCTCAAGATC	328
Db	274	TCAGGTAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGAAGTCTTTCACACTGAGAATC	333
QY	329	AACAGCCTCAGCCTGGAAGATTTTGGCAGTTATTACTGTCAACATTTTTCGGAGTACTCCG	388
Db	334	AGTAGAGTGGAGCTGAGGATGTGGGTGTTATTACTGTATGCAACATCTAGAAATATCCT	393
QY	389	TACACGTTCCGAGGGGGGACAAAGCTGGAATAAAACGGGCTGATGCTGCACCAACTGTA	448
Db	394	TTACAGTTTCAGTTCGGGGACAAAAGTTTGAANAATAACGGGCTGATGCTGCACCACTGTA	453
QY	449	TCCATCTTCCCAACATCCAGTGTAGCAGTGTAAACATCTGGAGGTGCCCTCAGTCTGTGCTTC	508
Db	454	TCCATCTTCCCAACATCCAGTGTAGCAGTGTAAACATCTGGAGGTGCCCTCAGTCTGTGCTTC	513
QY	509	TTGAACAACCTTCTACCCCAAGAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACA	568
Db	514	TTGAACAACCTTCTACCCCAAGAGACATCAATGTCAAGTGGAAAGATTGATGGCAGTGAACA	573
QY	569	CAAAATGGCGTCTGAAACAGTGTGACATGATCAGGACAGCAAAAGACAGACCTACAGCATG	628
Db	574	CAAAATGGCGTCTGAAACAGTGTGACATGATCAGGACAGCAAAAGACAGACCTACAGCATG	633
QY	629	AGCAGCACCTCAGCTTGACCAAGGACGAGTATGAACGACATTAACAGCTATACCTGTGAG	688
Db	634	AGCAGCACCTCAGCTTGACCAAGGACGAGTATGAACGACATTAACAGCTATACCTGTGAG	693
QY	689	GCCACTACAAGACATCAACTTCACCCATTGTCAGAGCTTCAACAGGAATGAGTGTAG	748
Db	694	GCCACTACAAGACATCAACTTCACCCATTGTCAGAGCTTCAACAGGAATGAGTGTAG	753
QY	749	AGACAAAGGTCTGAGAGCGCACACCACGCTCCCGAGCTCCACAGCTTCCCTCTCTAA	808
Db	754	AGACAAAGGTCTGAGAGCGCACACCACGCTCCCGAGCTTCCCTCTCTCTCTCTAA	813
QY	809	GGTCTTGGAGGCTTCCCGACAAAGGACCTACACTGTTCGGGTGCTCCAAACCTCTCTCC	868
Db	814	GGTCTTGGAGGCTTCCCGACAAAGGACCTACACTGTTCGGGTGCTCCAAACCTCTCTCC	873
QY	869	CACCT	928
Db	874	CACCT	933
QY	929	TATTCAATAAAGTGAGTCTTTGCA	952
Db	934	TATTCAATAAAGTGAGTCTTTGCA	957
RESULT 8			
AAQ94036			
D	AAQ94036	standard; cDNA; 952 bp.	
XX	AAQ94036;		
X			
X			
T	21-NOV-1995	(first entry)	
X	MAB 55.1	light chain cDNA.	

Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin; ss

[illegible]

Tue Jul 1 18:40:59 2003

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441 CAACGTATCCATCTTCCACCACATCCAGTCCAGTGAAGTGAAGTGCCTCAGTCG 500
428 CAACGTATCCATCTTCCACCACATCCAGTCCAGTGAAGTGAAGTGCCTCAGTCG 487
501 TGTGCTCTTGAACAACCTTACCCCAAAAGACATCAATGTCAAGTGAAGTGAAGTGC 560
488 TGTGCTCTTGAACAACCTTACCCCAAAAGACATCAATGTCAAGTGAAGTGAAGTGC 547
561 GTGAACACAAAATGGCGTCTGAAACAGTTGGACTGATCAGGACAGCAAGACGACCT 620
548 GTGAACACAAAATGGCGTCTGAAACAGTTGGACTGATCAGGACAGCAAGACGACCT 607
621 ACAGCATGAGCAGCAGCAGCAGCAGTGTGACCAAGGAGGATGTAAGCAGATACAGCTATA 680
608 ACAGCATGAGCAGCAGCAGCAGTGTGACCAAGGAGGATGTAAGCAGATACAGCTATA 667
681 CCTGTGAGGCCACTCACAAAGACATCAACTTCAACCATTTGTCAAGAGCTTCAACAGGAATG 740
668 CCTGTGAGGCCACTCACAAAGACATCAACTTCAACCATTTGTCAAGAGCTTCAACAGGAATG 727
741 AGTGTAGAGCAAAAGGTCCTGAGACGCGCCACCAAGGAGGATGTAAGCAGATACAGCTATACTT- 799
728 AGTGTAGAGCAAAAGGTCCTGAGACGCGCCACCAAGGAGGATGTAAGCAGATACAGCTATACTT 787
800 CCTTCTAGAGTCTTGGAGGCTTCCCAAGGAGGATGTAAGCAGATACAGCTATACTTCTCAAA 859
788 CCTTCTAGAGTCTTGGAGGCTTCCCAAGGAGGATGTAAGCAGATACAGCTATACTTCTCAAA 847
860 CCTTCTAGAGTCTTGGAGGCTTCCCAAGGAGGATGTAAGCAGATACAGCTATACTTCTCAAA 919
848 CCTTCTAGAGTCTTGGAGGCTTCCCAAGGAGGATGTAAGCAGATACAGCTATACTTCTCAAA 907
920 TGCAGAAAATATTCAATAAAGTGAGTCTTTG 950
908 TGCAGAAAATATTCAATAAAGTGAGTCTTTG 938

RESULT 9
AD28310
D AAD28310 standard; DNA; 5711 BP.
X AAD28310;
X AAD28310;
22-APR-2002 (first entry)
Alpha-lactalbumin (LA) Bot vector.
Regulatory element; vector; erythropoietin; growth hormone; insulin;
immunoglobulin; bone morphogenetic protein; interferon; interleukin;
superoxide dismutase; T-cell receptor; surface membrane protein;
viral antigen; transport protein; addressin; regulatory protein;
moloney murine leukemia virus; MoMuLV; bovine; alpha-lactalbumin;
human; promoter; double mutated pre-mRNA processing enhancer; PPE;
encephalomyocarditis virus; ECVV; internal ribosome entry site;
IRES; woodchuck RNA processing enhancer; WPRE; botulinum; ds.
Chimeric - Encephalomyocarditis virus.
Chimeric - Bos sp.
Chimeric - Homo sapiens.
Chimeric - Moloney murine leukemia virus.
Chimeric - Marmota monax.
Chimeric - Clostridium botulinum.
Chimeric - Unidentified.
Key Location/Qualifiers
misc_feature 1..2053
/tag= a
/region= "Bovine/human alpha-lactalbumin 5' flanking
region"
2093..2336
/tag= b
/region= "Double mutated PPE sequence"

```

```

FT CDS 2387..2443
FT /tag= c
FT /product= "cc49 signal peptide coding region"
FT CDS 2444..3088
FT /tag= d
FT /product= "Bot antibody light chain Fab coding region"
FT misc_feature 3112..3686
FT /tag= e
FT /note= "EMCV IRES"
FT CDS 3687..3745
FT /tag= f
FT /product= "Bovine alpha-lactalbumin signal peptide
coding region"
FT CDS 3746..4443
FT /tag= g
FT /product= "Bot antibody heavy chain Fab coding region"
FT misc_feature 4481..5072
FT /tag= h
FT /note= "WPRE sequence"
FT LTR 5118..5711
FT /tag= i
FT /note= "MoMuLV 3' LTR"
WO200202783-A2.
10-JAN-2002.
29-JUN-2001; 2001WO-US20714.
03-JUL-2000; 2000US-21585LP.
(GALA-) GALA DESIGN INC.
Bleck GT;
WPI; 2002-154749/20.
Novel regulatory elements including nucleic acid encoding hybrid
alpha-lactalbumin promoter or mutant RNA export element, for expressing
one or more proteins e.g. antibodies, pharmaceutical proteins in host
cells
Example 1; Fig 11; 151pp; English.
The invention relates to novel regulatory elements and vectors for the
expression of one or more proteins in a host cell. The invention further
provides methods of indirectly detecting the expression of a protein of
interest, comprising providing the host cell transfected with a vector
encoding a polyclonistic sequence comprising a signal protein and a
desired protein operably linked by an internal ribosome entry site
(IRES), and culturing the host cell under suitable conditions so that
the signal protein and the desired protein is produced, where the
presence of signal protein indicates the presence of desired protein.
Regulatory elements and vectors of the invention are useful for the
expression of proteins of interest in a host cell. They are useful for
producing an immunoglobulin (Ig), preferably secretory Ig. They are
useful in the expression of one or more proteins such as erythropoietin,
growth hormone, insulin, immunoglobulins, protein C, cytokines and their
receptors, hormones, Von Willebrand's factor, lung surfactant, serum
albumins, DNase, vascular endothelial growth factor, receptors for
hormones or growth factors, rheumatoid factors, nerve growth factors,
CD proteins, osteoinductive factors, immunotoxins, bone morphogenetic
protein, interferons, colony stimulating factors, interleukins,
superoxide dismutase, T-cell receptors, surface membrane proteins,
viral antigens, transport proteins and their fragments. The vectors are
antibodies, chimeric proteins and their fragments. The vectors are
particularly useful for expressing G protein coupled receptors and other
transmembrane proteins. The retroviral vectors are useful for expressing
proteins in mammalian tissue culture host cells, including rat fibroblast
cells, bovine kidney cells and human kidney cells. The present sequence
is alpha lactalbumin (LA) Bot vector used in the invention. The vector
comprises the following elements: bovine/human alpha-lactalbumin hybrid
promoter, double mutated pre-mRNA processing enhancer (PPE) sequence:

```

cc49 signal peptide, botulinum toxin antibody light chain, IRES from
encephalomyocarditis virus (ECMV), bovine alpha-lactalbumin signal
peptide, botulinum toxin antibody heavy chain, woodchuck mRNA processing
enhancer (WPRE) sequence and 3' moloney murine leukemia virus (MOMLV)
LTR.

Query Match		64.8%	Score 634.2;	DB 24;	Length 5711;
Best Local Similarity		90.8%	Pred. No. 1.2e-119;		
Matches 675; Conservative		0;	Mismatches 68;	Indels	Gaps 0;
QY	61	GTCTCGGGCTGCTCTGCTGCTGGGTATACAGTGGCAGATGTGACATCCAGATGACTCA	120		
Db	2401				
QY	121	GTCTCCAGCTCCCTATCTGCATCTGTGGGAGAACTGTCAACATCACATGTGCGACGAAG	180		
Db	2461	GTCTCCAGCTCCCTATCTGCATCTGTGGGAGAACTGTCACTATCACATGTGCGACGAAG	2520		
QY	181	TGGGAATATTCAAAATATTTAGCATGTTATCAGCAGACACAGGGGAAAATCTCTCAGCT	240		
Db	2521	TGGGAATATTCAAATATTTAGCATGTTATCAGCAGAAACAGGAAAAATCTCTCAGCT	2580		
QY	241	CCTGCTATTCTTGC AAAACCTTAGCAGATGGTGGCCATCAAGGTTCACTGGCAGTGG	300		
Db	2581				
QY	301	ATCAGGACACAATATTTCTCAAGATCAACAGCCTGCAGCTGAAGATTTTGGCAGTTA	360		
Db	2641	ATCAGGACACAATATTTCTCAAGATCAACAGCCTGCAGCTGAAGATTTTGGGAGTTA	2700		
QY	361	TTACTGTCAACATTTTGGAGTACTCTCTACAGTTCTGAGGGGGGACCAAGCTGAAAT	420		
Db	2701				
QY	421	AAACGGGCTGATCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAAC	480		
Db	2761	CAAACGGGCTGATCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAAC	2820		
QY	481	ATCTGAGGTGCCTCAGTCTGTGCTTCTTGACAACTTCTACCCCAAAGACATCAATGT	540		
Db	2821	ATCTGAGGTGCCTCAGTCTGTGCTTCTTGACAACTTCTACCCCAAAGACATCAATGT	2880		
QY	541	CAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCTGAACAGTTGGACTGATCA	600		
Db	2881	CAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCTGAACAGTTGGACTGATCA	2940		
QY	601	GGACGCAAGACAGCAGCTTACAGCATGACAGACCCCTCACCTTGACCAAGGACGAGTA	660		
Db	2941	GGACGCAAGACAGCAGCTTACAGCATGACAGACCCCTCACATTTGACCAAGGACGAGTA	3000		
QY	661	TGAACGACATAACAGTATACCTGTGAGGCCACTCAAGACATCAACTTCACCCATTGT	720		
Db	3001	TGAACGACATAACAGTATACCTGTGAGGCCACTCAAGACATCAACTTCACCCATTGT	3060		
QY	721	CAAGAGCTTCAACGGAATGAGTGTGAGAGCAAAAGTCTCTGAGAGCCACCAACAGCTTC	780		
Db	3061	CAAGAGCTTCAACGGAATGAGTGTGAGAGCAAAAGTCTCTGAGAGCCACCAACAGCTTC	3120		
QY	781	CCAGCTCCATCTATCTTCCT 803			
QY	3121	CTCCCCCCCCCTTAACGTTACT 3143			

RESULT 10

AD28276

AAD28276 standard; DNA; 6255 BP.

AAD28276;

22-APR-2002 (first entry)

22-APR-2002 (first entry)

[illegible]

LNBOTDC vector #1.	
Bovine; alpha-lactalbumin; pharmaceutical; industrial; ECMV; IRES encephalomyocarditis virus; diagnostic; internal ribosome entry s screening; cytomegalovirus; moloney murine leukemia virus; MoMuLV botulinum; ds.	
Chimeric - Encephalomyocarditis virus. Chimeric - Clostridium botulinum. Chimeric - Moloney murine leukemia virus. Chimeric - Bos sp. Chimeric - Cytomegalovirus. Chimeric - Unidentified.	
Key	Location/Qualifiers
LTR	1..589 /*tag= a /note= "MoMuLV 5' LTR"
misc_feature	659..1468 /*tag= b /note= "MoMuLV Extended packaging region"
misc_feature	1512..2306 /*tag= c /note= "Neomycin resistance gene"
promoter	2656..3473 /*tag= d /note= "CMV promoter"
CDS	3516..3572 /*tag= e /product= "cc49 signal peptide coding region"
misc_feature	3573..4217 /*tag= f /note= "Bot Fab 5 light chain"
misc_feature	4235..4816 /*tag= g /note= "EMCV IRES"
CDS	4817..4873 /*tag= h /product= "Modified bovine alpha-1A signal peptide coding region"
misc_feature	4874..5572 /*tag= i /note= "Bot Fab 5 heavy chain"
LTR	5662..6255 /*tag= j /note= "MoMuLV 3' LTR"
WO200202738-A2.	
10-JAN-2002.	
29-JUN-2001; 2001WO-US20710.	
03-JUL-2000; 2000US-215925P.	
(GALA-) GALA DESIGN INC.	
Bremel RD, Miller LU, Black GT, York D;	
WPI; 2002-154737/20.	
Host cell for producing a desired protein and for screening compound useful for pharmaceutical, industrial, diagnostic and other purposes comprises multiple integrating vectors having an exogenous gene - Example 3; Fig 15; 19lpp; English.	

Host cell for producing a desired protein and for screening compounds useful for pharmaceutical, industrial, diagnostic and other purposes, comprises multiple integrating vectors having an exogenous gene -
Example 3; Fig 15; 19pp; English.

The invention relates to a host cell comprising a genome having at least two integrated integrating vectors. The integrating vectors comprise at least one exogenous gene operably linked to a promoter. The host cell is useful for producing a desired protein and for comparing protein functions. The host cells comprises a reporter gene which is from gene fluorescent protein, luciferase, beta-galactosidase and beta-lactamase.

and the assaying step further comprises detecting a signal from the reporter gene. The desired protein includes protein for pharmaceutical, industrial, diagnostic and other purposes. The host cells is useful for indirectly detecting the expression of a desired protein, comprising providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein operably linked by an internal ribosome entry site (IRES), and culturing the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein indicates the presence of desired protein. The present sequence is LNBORC vector used in the invention. The vector comprises the following elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV extended viral packaging region, neomycin phosphotransferase gene, CMV promoter, cc49 signal peptide coding region, Bot Fab 5 light chain, IRES sequence from encephalomyocarditis virus (ECMV), modified bovine alpha-lactalbumin signal peptide coding region, Bot Fab5 heavy chain, and moloney murine leukemia virus (MoMuLV) 3' LTR.

	Sequence	6255 BP;	1433 A;	1741 C;	1607 G;	1474 T;	0 other;
Query Match		64.8%;	Score 634.2;	DB 24;	Length 6255;		
Best Local Similarity		90.8%;	Pred. No. 1.2e-119;				
Matches		675;	Conservative 0;	Mismatches 68;	Indels 0;	Gaps 0;	
/							
3	61	GGTCCTGGCGTTCGTGCTGCTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA	120				
3	3530	GGTCCTTCCTTCCTCCTGCAGTAACACAGGTGCCATCCGACATCCAGTAAGACCCA	3589				
Y	121	GNCTCCAGCCTCCCTATCTGCATCTCTGGAGAGAACTGTCAACCATCACATGTGCAGCAAG	180				
b	3590	GTCTCCAGCCTCCCTATCTGCATCTCTGGAGAGAACTGTCACTATCACATGTGCAGCAAG	3649				
Y	181	TGGGATATTCAAAAATTATTAGCATGGTATCAGCAGACACAGGGAAAAATCTCTCTCAGCT	240				
b	3650	TGGGAATATTCACAAATTTATGCAATTTTASCATGGTATCAGCAAAACAGGGAAAAATCTCTCAGCT	3709				
Y	241	CTGTGCTATTTCTGCAAAAACCTTTAGCAGATGGTGTGCCATCAGGTTTCAGTGGCAGTGG	300				
b	3710	CTGTGCTATAATGCAAAAACCTTTAGCAGATGGTGTGCCATCAGGTTTCAGTGGCAGTGG	3769				
Y	301	ATCAGGNACACATATTTCTCTCAAGATCAACAGCCTGCAGCCTCAAGATTTTGGAGTTA	360				
b	3770	ATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTCAAGATTTTGGAGTTA	3829				
Y	361	TTACTGTCAACATTTTTTGGAGTACTCCGTACACGTTGGAGGGGGGACCAGCTGGGAAT	420				
b	3830	TTACTGTCAACATTTTTTGGAGTACTCCGTGACGCTTCGGTGGAGGCACCAAGCTGGAAT	3889				
Y	421	AAACGGGCTGATGCTGGACCAACTGTATCCATCTTCCACCATCCAGTGGACAGTTAAC	480				
b	3890	CAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGGACAGTTAAC	3949				
Y	481	ATCTGGAGGTCCTCAGTCGTGTGCTTCTTGAAACAATTTTACCCCAAGACATCAATGT	540				
b	3950	ATCTGGAGGTCCTCAGTCGTGTGCTTCTTGAAACAATTTTACCCCAAGACATCAATGT	4009				
Y	541	CAAGTGGAGATTTGATGGCAGTGAACGACAAATGGCTCCTGAACAGTTGGACTGATCA	600				
b	4010	CAAGTGGAGATTTGATGGCAGTGAACGACAAATGGCTCCTGAACAGTTGGACTGATCA	4069				
Y	601	GGACAGCAAGACAGCACACCTACAGCATGAGCAGCACCCCTCAGCTTGACCAAGACAGTA	660				
b	4070	GGACAGCAAGACAGCACACCTACAGCATGAGCAGCACCCCTCAGCTTGACCAAGACAGTA	4129				
Y	661	TGAACGCATTAACAGCTATACCTGTGAGGCCACTACAAGACATCAACTTCACCCATTGT	720				
b	4130	TGAACGCATTAACAGCTATACCTGTGAGGCCACTACAAGACATCAACTTCACCCATTGT	4189				
Y	721	CAAGAGCTTCAACAGGAATGAGTTGAGACAAAGGTCCTGAGAGCCCAACCAACCAAGCTC	780				
b	4190	CAAGAGCTTCAACAGGAATGAGTTGAAAGCATCGATTTCCCGTGAATTCGCCCTCTC	4249				
	781	CCAGAGCTTCACTATCTTCCCT	803				

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Db      4250 CCTCCCCCCCCCTTAACGTTACT 4272
      || || || ||||| || || ||
RESULT 11
AAD28315 AAD28315 standard; DNA; 6255 BP.
XX
XX
AC AAD28315;
XX
XX 22-APR-2002 (first entry)
XX
XX LNBOTDC vector #1.
XX
XX Regulatory element; vector; erythropoietin; growth hormone; insulin;
KW immunoglobulin; bone morphogenetic protein; interferon; interleukin;
KW superoxide dismutase; T-cell receptor; surface membrane protein; ECMV;
KW viral antigen; transport protein; addressin; regulatory protein; IRES;
KW bovine; alpha-lactalbumin; CMV; encephalomyocarditis virus; MoMuLV;
KW internal ribosome entry site; cytomegalovirus; botulinum;
KW moloney murine leukemia virus; ds.
XX
XX Chimeric - Encephalomyocarditis virus.
OS
OS Chimeric - Clostridium botulinum.
OS
OS Chimeric - Moloney murine leukemia virus.
OS
OS Chimeric - Bos sp.
OS
OS Chimeric - Cytomegalovirus.
OS
OS Chimeric - Unidentified.
XX
XX
FH Key Location/Qualifiers
FT LTR 1..589
FT /*tag= a
FT /*note= "MoMuLV 5' LTR"
FT misc_feature 659..1468
FT /*tag= b
FT /*note= "MoMuLV Extended packaging region"
FT misc_feature 1512..2306
FT /*tag= c
FT /*note= "Neomycin resistance gene"
FT promoter 2656..3473
FT /*tag= d
FT /*note= "CMV promoter"
FT CDS 3516..3572
FT /*tag= e
FT /*product= "Cc49 signal peptide coding region"
FT misc_feature 3573..4217
FT /*tag= f
FT /*note= "Bot Fab 5 light chain"
FT misc_feature 4235..4816
FT /*tag= g
FT /*note= "EMCV IRES"
FT CDS 4817..4873
FT /*tag= h
FT /*product= "Modified bovine alpha-LA signal peptide coding region"
FT misc_feature 4874..5572
FT /*tag= i
FT /*note= "Bot Fab 5 heavy chain"
FT LTR 5662..6255
FT /*tag= j
FT /*note= "MoMuLV 3' LTR"
XX
XX WO200202783-A2.
XX
XX 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US20714.
XX
XX 03-JUL-2000; 2000US-215851P.
XX
XX (GALA-) GALA DESIGN INC.
XX
XX Bleck GT;

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this invention binds to the non-neurotoxic proteins that are found in neurotoxin complexes A and B. Such antibody fragments are able to act as immunosensors for detecting botulinum toxins in food and are also useful in health care and in military applications. They are less expensive to produce than monoclonal antibodies as they can be isolated from large scale bacterial cultures. Also, the affinity of an rFab may be altered by mutagenesis of its gene and subsequent screening of the expressed rFabs.

SQ Sequence 1644 BP; 438 A; 446 C; 402 G; 358 T; 0 other;

Query Match 63.9%; Score 626; DB 20; Length 1644;
Best Local Similarity 92.9%; Pred. No. 4.6e-118;
Matches 656; Conservative 0; Mismatches 50;

	Y	51	TGCTCACTACAGTCTCGGTGGTTGCTGCCTTGAGGTGCCAGATGTCATCC	110
	b	101	TGCCTAGCGCGCGCTGGATTGTTATTACTCGCTGCCAACCGCATCGCGCAGATCC	160
	Y	111	AGATGACTCAGTCTCCAGCCCTCCCTATCTGCATCTGTGGGAAGAACTGTCCACATCACAT	170
	b	161	AGATGACCCAGTCTCCAGCCCTCCCTATCTGCATCTGTGGGAAGAACTGTCACTATCACAT	220
	Y	171	GTCAGAGAAGTGGGAATAATCAAATAATTAGCATGGTATCAGCAGACACAGGGAAT	230
	b	221	GTCAGAGAAGTGGGAATAATCACAATTAATTAGCATGGTATCAGCAGAAACAGGGAAT	280
	Y	231	CTCCTCAGCTCTGGTCTATTTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA	290
	b	281	CTCCTCAGCTCTGGTCTATAAATCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA	340
	Y	291	GTGGCAGTGATCAGGAACACAAATATTTCTCAAGATCAACAGCCTGCAGCCTGNAGATT	350
	b	341	GTGGCAGTGATCAGGAACACAAATATTTCTCAAGATCAACAGCCTGCAGCCTGNAGATT	400
	Y	351	TTGGGAGTTATTACTGTCAACATTTTTGGAGTATCCGTACACGTTCCGAGGGGGACCA	410
	b	401	TTGGGAGTTATTACTGTCAACATTTTTGGAGTATCCGTACACGTTCCGAGGGGGACCA	460
	Y	411	AGCTGGAATAAAACGGGTGATGCTCACCAACTGATCCATCTTGAACAATCTTACCCTCAAG	530
	b	461	AGCTGGAATAAAACGGGTGATGCTCACCAACTGATCCATCTTGAACAATCTTACCCTCAAG	520
	Y	471	ACAGTTACATCTCGAGGTGCCCTCAGTCGTGTCTTGAACAATCTTACCCTCAAG	580
	b	521	ACAGTTACATCTCGAGGTGCCCTCAGTCGTGTCTTGAACAATCTTACCCTCAAG	590
	Y	531	ACATCAATGTCAAGTGGAGAATTGATGGCAGTGAAGCAGAAAAATGGCGTCTGAACAGTT	590
	b	581	ACATCAATGTCAAGTGGAGAATTGATGGCAGTGAAGCAGAAAAATGGCGTCTGAACAGTT	640
	Y	591	GGACTGATCAGACAGCAAGACAGACCTACAGCATGAGCAGCCCTCACGTTGACCA	650
	b	641	GGACTGATCAGACAGCAAGACAGACCTACAGCATGAGCAGCCCTCACGTTGACCA	700
	Y	651	AGGAGGATATCAACGACATACAGCTATACCTGTGAGGCCACTACAAGACATCAACTT	710
	b	701	AGGAGGATATCAACGACATACAGCTATACCTGTGAGGCCACTACAAGACATCAACTT	760
	Y	711	CACCCATTGTCAAGAGCTTCAACAGGAATGAGTTAGACAAAG	756
	b	761	CACCCATTGTCAAGAGCTTCAACAGGAATGAGTTAGACAAAG	806

SULT 14
X86664

AAX86664 standard; cDNA; 1672 BP.

AAx86664;

20-OCT-1999 (first entry)

Murine anti-botulinum toxin antibody fragment (BotFab 5) cDNA.

XX	Recombinant antibody fragment; rFab; botulinum; neurotoxin;	
KW	Clostridium botulinum; detection; ds.	
XX		
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	117..827
FT		/tag= a
FT		/product= "BotFab 5 antibody fragment, light chain"
FT	CDS	847..1611
FT		/tag= b
FT		/product= "BotFab 5 antibody fragment, heavy chain"
XX		
PN	US5932449-A.	
XX		
PD	03-AUG-1999.	
XX		
PF	30-JAN-1997; 97US-0792824.	
XX		
PR	01-FEB-1996; 96US-0011013.	
PR	30-JAN-1997; 97US-0792824.	
XX		
PA	(USSA) US SEC OF ARMY.	
XX		
PI	Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;	
XX		
DR	WPI: 1999-492692/41.	
DR	P-PSDB; AAY30116, AAY30117.	
XX		
PT	Detection of botulinum toxin	
XX		
PS	Claim 4; Columns 13-18; 24pp; English.	
XX		
CC	This sequence represents the cDNA coding for the light and heavy chain of BotFab 5, a murine recombinant antibody fragment (rFab) specific to botulinum toxin types A and B. A cDNA library was made from mouse mRNA isolated from mice immunised with human pentavalent toxoid. The clone mouse heavy and light chains were expressed in phage display libraries and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum neurotoxin is produced as several antigenically distinct serotypes (A-G) and is non-covalently associated with non-neurotoxic proteins. The rFab of this invention binds to the non-neurotoxic proteins that are found in neurotoxin complexes A and B. Such antibody fragments are able to act as immunosensors for detecting botulinum toxins in food and are also useful in health care and in military applications. They are less expensive to produce than monoclonal antibodies as they can be isolated from large scale bacterial cultures. Also, the affinity of a rFab may be altered by mutagenesis of its gene and subsequent screening of the expressed rFabs.	

SQ Sequence 1672 BP; 439 A; 452 C; 403 G; 378 T; 0 other;

Query Match 63.9%; Score 626; DB 20; Length 1672;
Best Local Similarity 92.9%; Pred. No. 4.6e-118;
Matches 55

556; Conservative	0; Mismatches	50; Indels	0; Gaps	0;
51	TGCTCACTCAGTCTCGGCGTTGCTGCTGCTGCGCTTACAGTGCAGATGTGCATCC	110		
130	TGCTTACGGCGCGCTGATTGTTATTAATCGCTGCCCAACCGACGATGGCGGACATCC	189		
111	AGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAACTGTGCACCATCACAT	170		
190	AGATGACCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAACTGTGCATCTATCACAT	249		
171	GTCGAGCAAGTGGGAATATTCAAATTTATTAGCATGGTATCAGCAGACACAGGGAAT	230		
250	GTCGAGCAAGTGGGAATATTCAAATTTATTAGCATGGTATCAGCAGAAACAGGGAAT	309		
231	CTCCTCAGCTCCTGGTCTATTTCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGTTCA	290		
310	CTCCTCAGCTCCTGGTCTATTAATGCAAAACCTTAGCAGATGGTGTGCCATCAAGTTCA	369		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 23, 2003, 16:26:36 ; Search time 2633.04 Seconds
(without alignments)
10820.814 Million cell updates/sec

Title: US-09-770-916-3

Perfect score: 979

Sequence: 1 accaccttctgagtcag.....aaaaaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_ph.*
24: em_pl.*
25: em_ro.*
26: em_sts.*
27: em_un.*
28: em_vi.*
29: em_vt.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_mus.*
33: em_htg_other.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	898	91.7	954	10	BC002112	BC002112 Mus muscu
2	881.2	90.0	942	10	BC019474	BC019474 Mus muscu
3	821	83.9	885	10	MMIG6L	X13187 Mouse mRNa
4	755	77.1	959	10	BC015292	BC015292 Mus muscu
5	751.8	76.8	1019	10	BC027418	BC027418 Mus muscu
6	751.8	76.8	1038	10	BC013496	BC013496 Mus muscu
7	751.6	76.8	972	10	AF466770	AF466770 Mus muscu
8	739.6	75.5	931	10	MMIG15K	X56394 Mouse mAB-1
9	733.6	74.9	998	9	S65921	S65921 anti-colore
10	689	70.4	721	10	MMU56412	U56412 Mus musculu
11	685.8	70.1	721	10	MMU56413	U56413 Mus musculu
12	685.4	70.0	943	10	MUSIGKAJ	J00560 mouse ig ka
13	683.8	69.8	943	10	MMIGK9	V00810 M.musculus
14	683.6	69.8	977	10	BC002035	BC002035 Mus muscu
15	679	69.4	974	10	MMABMST2	X79906 M.musculus
16	678.6	69.3	963	10	BC021781	BC021781 Mus muscu
17	677	69.2	882	6	E00398	E00398 Mouse anti-
18	672.8	68.7	985	10	MUSIGKBAA	M63550 Mouse Ig re
19	669.6	68.4	943	10	BC028540	BC028540 Mus muscu
20	669.6	68.4	974	10	BC019760	BC019760 Mus muscu
21	666.2	68.0	956	10	MMKAPLI	X87231 M.musculus
22	666.2	68.0	1008	10	BC031498	BC031498 Mus muscu
23	665.6	68.0	957	10	MMU65535	U65535 Mus musculu
24	664.6	67.9	938	10	MMIGKL	X02816 Mouse mRNa
25	663.2	67.7	969	10	BC006643	BC006643 Mus muscu
26	654.4	66.8	993	10	AF466768	AF466768 Mus muscu
27	652	66.6	961	6	E08433	E08433 cDNA encodi
28	650.6	66.5	920	10	MMTWIIGK	X67211 M.musculus
29	650.6	66.5	940	6	A44968	A44968 Sequence 24
30	650.6	66.5	940	6	I64459	I64459 Sequence 24
31	649.4	66.3	1034	10	BC028925	BC028925 Mus muscu
32	649.2	66.3	882	10	MMIGLAKA	X70424 M.musculus
33	634.2	64.8	5711	6	AX359934	AX359934 Sequence
34	634.2	64.8	5711	6	AX382148	AX382148 Sequence
35	634.2	64.8	6255	6	AX359939	AX359939 Sequence
36	634.2	64.8	6255	6	AX382153	AX382153 Sequence
37	620.8	63.4	927	10	MUSIIC	DI7386 mRNa for mo
38	615.6	62.9	943	6	A22259	A22259 M.musculus
39	615.6	62.9	943	6	A77136	A77136 Sequence 4
40	615.6	62.9	943	6	AR029101	AR029101 Sequence
41	615.6	62.9	943	6	E33133	E33133 Humanized a
42	607.8	62.1	645	10	AF290569	AF290569 Mus muscu
43	598	61.1	882	6	A78883	A78883 Sequence 3
44	597.6	61.0	652	10	MSU00929	U00929 Mus MRL/lpr
45	593.8	60.7	862	10	RNU39609	U39609 Rattus norv

ALIGNMENTS

RESULT 1
BC002112
LOCUS
DEFINITION BC002112 954 bp mRNA linear ROD 07-AUG-2002
Mus musculus, Similar to immunoglobulin kappa chain variable 8
(V8), clone MGC:6612 IMAGE:3488780, mRNA, complete cds.
ACCESSION BC002112
VERSION BC002112.1 GI:12805290
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 954)
AUTHORS Strausberg R.
TITLE Direct Submission

Pred. No. is the number of results predicted by chance to have a

JOURNAL
Submitted (31-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grinstead, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 7 Row: k Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

[illegible]

RESULT 2	
BC019474	
LOCUS	942 bp mRNA linear ROD 07-AUG-2002
DEFINITION	Mus musculus, clone MGC:28604 IMAGE:4217320, mRNA, complete cds.
ACCESSION	BC019474
VERSION	BC019474.1 GI:18044484
KEYWORDS	MGC.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS	1 (bases 1 to 942)
TITLE	Strausberg,R.
JOURNAL	Direct Submission Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amd@bcm.tmc.edu

Tue Jul 1 18:40:58 2003

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497 TACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAATGGCGTC 556
581 CTGAACAGTTGGAGTATCAGGACAGCAAGACAGCAGCTACAGCATGAGCAGCAGCCTC 640
557 CTGAACAGTTGGAGTATCAGGACAGCAAGACAGCAGCTACAGCATGAGCAGCAGCCTC 616
641 ACCTTGACCAAGGAGGATGAACGACATGAACAGTATACCTGTGAGGCCACTCACAAG 700
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821 TTCCCCACAAAGGAGCTTACACTGTTCGGGTGCTCCAAACCTCCTCCCACTCCTCTTC 880
797 TTCCCCACAAAGGAGCTTACACTGTTCGGGTGCTCCAAACCTCCTCCCACTCCTCTTC 856
881 CTCCTCCTCCTTCTCCTTCTTATCATGCTTAATTTGCGAGAAATATTTCAATTAAG 940
857 CTCCTCCTCCTTCTCCTTCTTATCATGCTTAATTTGCGAGAAATATTTCAATTAAG 916
941 TGAGTCTTTGCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAA 979
917 TGAGTCTTTGCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAA 955

RESULT 6
LOCUS BC013496 1038 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, clone IMAGE:4219618, mRNA, partial cds.
ACCESSION BC013496
VERSION BC013496.1 GI:15488700
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus; Craniata; Chordata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1038)
Strausberg, R.
Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: FRAC Plate: 25 Row: a Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
Location/Qualifiers
1..1038
/organism="Mus musculus"
/db_xref="taxon:10090"
FEATURES
source

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/clone="IMAGE:4219618"
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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
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/codon_start=2
/product="unknown (protein for IMAGE:4219618)"
/db_xref="id:AAH13496.1"
/translation="GRVGRPTPLLLCFQGRCDIQMTQTSSLSASLGRVITSCSG
SQGLANLWYQOKPDGTGKLLIYYTSLHSGVPSRFSGSAGTGYSLTINLEPDI
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KDINVKIKDGSERQNGVLSWTDDQSDSTYSMSSTLTITKDEYHRHNSYTCEATHK
TSTSPIVKSFNNEC"
BASE COUNT 371 a 253 c 192 g 222 t
ORIGIN
Query Match 76.8%; Score 751.8; DB 10; Length 1038;
Best Local Similarity 89.3%; Pred. No. 9e-198;
Matches 810; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
73 GCTGCTGCTGTGCTTACAGTGCAGATGTCACCATCATCTGCGAGCAAGTGGGAATATTC 132
28 GCTGCTGCTGTGCTTACAGTGCAGATGTCACCATCATCTGCGAGCAAGTGGGAATATTC 87
133 CCTATCTGCATCTGTGGGAGAAACTGTCACCATCATCTGCGAGCAAGTGGGAATATTC 192
88 CCTGCTGCTGCTTCTGCGAGCAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 147
193 AAATTATTAGCATGTTATCAGCAGACACAGGAGAAATCTCCTCAGCTCCTCGTCTATTC 252
148 CAATTATTAACTGGTATCAGCAAAACCCAGATGGAACCTGTTAACTCCTGATCTATTA 207
253 TGCAGCAACCTTACAGATGCTGCGCATCAAGTTCAGTGGCAGTGGATGAGCAACACA 312
267 TATTTCTCTACCATCAGCAACCTGGAACCTGGAATATTTGCACTTACTATTTGACGA 267
313 ATATTCTCTCAAGATCAACAGCTGCAGCCTGGAAGATTTGGGGATTATTTACTGTCACA 372
268 TATTTCTCTACCATCAGCAACCTGGAACCTGGAATATTTGCACTTACTATTTGACGA 327
373 TTTTGGAGTACTCGGTACACGTTCCGAGGGGGGAGGAGTGGAAATATAAAGGGCTGA 432
328 GTATGCTTACCTTCCGTGGAGCTTGGTGGAGGACCAAGTGGAAATATAAAGGGCTGA 387
433 TGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGCAGTGCAGTGCAGTGCAGTGC 492
388 TGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGCAGTGCAGTGCAGTGCAGTGC 447
493 CTCAGTCTGCTGCTTCTTGAACAACTTCTACCCAAAGACATCAATGTCAGTGGAGAT 552
448 CTCAGTCTGCTGCTTCTTGAACAACTTCTACCCAAAGACATCAATGTCAGTGGAGAT 507
553 TGATGGCAGTGAACGACAAATGCGTCTCTGACAGTTCGAGTTCGAGTTCGAGTTCGAG 612
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613 CAGCACCTTACAGCATGAGCAGCAGCTTACAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 672
568 CAGCACCTTACAGCATGAGCAGCAGCTTACAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 627
673 CAGCTATACCTTGTGAGGCCACTCACAAGACATCAACTTTCACCCCAATTTGTCAGAG 732
628 CAGCTATACCTTGTGAGGCCACTCACAAGACATCAACTTTCACCCCAATTTGTCAGAG 687
733 CAGGAATGAGTGTAGACAAAGTCTCTGAGCAGCCACCACTCCAGCTCCAGCTCCATC 792
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793 CTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAACAGCGAGCTTACCACTGTTGGG 852
748 CTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCAACAGCGAGCTTACCACTGTTGGG 807

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Db	338	CAAGAAGATGTTGCCATCTACTTTTGCCAACAGGGTTATACGCTTCCTGTACAGTTCGA	397
QY	401	GGGGGACCAAGCTTGGAAATAAAGGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA	460
Db	398	GGGGGACCAAGCTTGGAAATAAAGGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA	457
QY	461	CCATCCAGTGTAGCAGTTAAACATCTTGGAGTGCCCTCAGTCGTTGCTTCTTGAACAATTC	520
Db	458	CCATCCAGTGTAGCAGTTAAACATCTTGGAGTGCCCTCAGTCGTTGCTTCTTGAACAATTC	517
QY	521	TACCCCAAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGGCGTC	580
Db	518	TACCCCAAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGGCGTC	577
QY	581	CTGAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCTC	640
Db	578	CTGAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCTC	637
QY	641	ACCTTGACCAAGGACGAGTAGTGAACGACATTAACAGCTATACCTGTGAGGCCACTACAAG	700
Db	638	ACCTTGACCAAGGACGAGTAGTGAACGACATTAACAGCTATACCTGTGAGGCCACTACAAG	697
QY	701	ACATCAACTTCACCCCATTTGTCAGAGCTTCAACAGGAATGAGTGTAGACAAAAGTCC	760
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QY	761	TGAGAGGCCACCAACAGCTCCCGAGCTCCATCTTCCCTTCAAGGTCTTGAGGC	820
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Db	878	CTCCTCCCTCCCTTCTGGCTTTTATCATGCTAATATTGTCAGAAAATPATTCAATAAG	937
QY	941	TGAGTCTTTTGCAAAAAAATAAAAAAATAAAAAA 975	
Db	938	TGAGTCTTTTGCAAAAAAATAAAAAAATAAAAAA 972	
RESULT 8			
MMIG15K			
LOCUS		931 bp	linear
DEFINITION		Mouse MAB-1505 mRNA for immunoglobulin kappa chain.	ROD 23-MAR-1995
ACCESSION		X56394	
VERSION		X56394.1 GI:51622	
KEYWORDS		gamma-immunoglobulin; immunoglobulin.	
SOURCE		Mus musculus.	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		1 (bases 1 to 931)	
TITLE		Vandamme.A.M.I.	
JOURNAL		Direct Submission	
REFERENCE		Submitted (06-JUL-1990) Vandamme A.M.I., University of Leuven, Center for Thrombosis and Vascular Research, Herestraat 49, B-3000 Leuven	
AUTHORS		2 (bases 1 to 931)	
TITLE		Vandamme.A.M., Bulens.F., Bernar.H., Nelles,L., Lijnen,R.H. and Collen,D.	
JOURNAL		Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer	
MEDLINE		Eur. J. Biochem. 192 (3), 767-775 (1990)	
PUBMED		9106173	
COMMENT		2209622	
		rearranged;	
		Zapi;	

This sequence is of c DNA corresponding tomRNA for the antibody
MA1515 directed against crosslinked human fibrin fragment D-dimer
Data kindly reviewed (27-NOV-1990) by Vandamme A.M.

FEATURES

source

Location/Qualifiers

1..931

/organism="Mus musculus"

/strain="BALB/c"

/isolate="MA15C5"

/db_xref="taxon:10090"

/chromosome="chromosome 12"

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/cell_line="hybridoma 15C5"

/cell_type="myeloma hybridoma (P3X63-Ag.8-6.5.3)"

/tissue_type="plasma"

/clone_lib="lambda gt11, lambda"

5..709

/note="15C5 Ig kappa precursor"

/codon_start=1

/protein_id="CAA39805.1"

/db_xref="GI:51623"

/translation="MRTPAQFLGILLWFFPKIKDKWTQSPSSWYASLGERVTWICK
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PKDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTLLTKDEYERHNSYTCEATH
KTSTSPIVKSFNRNEC"

5..64

sig_peptide

V_region

V_segment

C_region

BASE COUNT 258 a 240 c 202 g 231 t

ORIGIN

Query Match

Best Local Similarity

Matches 811; Conservative

0; Mismatches 119; Indels 0; Gaps 0;

75.5%; Score 739.6; DB 10; Length 931;

41 GTCATGAGTGTCTCACTCAGGTCCTGGGCTGCTGCTGTGGCTTACAGTGCCAGA 100

2 GACATGAGGACCCCTCTCAGTTCTTGGAACTTGTGCTCTGGTTCCAGGTATCAA 61

101 TGTACATCAGATGACTAGTCTCCAGCCTCCCTATCTGCTATCTGTGGGAACTGTC 160

62 TGTGACATCAAGATGACCCAGTCTCCATCTTCCATGTATGATCTCTAGGAGAGAGTC 121

161 ACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTTATAGCATGTTATCAGACACA 220

122 ACTGTCACTTGCAGGGGAGTCAGGACATTAATAGCTATTAAAGCTGGATCCAGACAAA 181

221 CAGGGAATACTCTCAGCTCTGCTATCTTCGCAAAACCTTAGCAGATGGTGTGCCA 280

182 CCAGGGAATCTCTCAAGACCCCTGATCTACCGTGGAAACAGATTGGTTGTGGGTCCCA 241

281 TCAAGTTTCAGTCAGTCAGTGGATCAGGACAAATATCTCTCAAGATCAACAGCCTGCAG 340

242 TCAAGTTTCAGTCAGTCAGTGGATCAGGACAAATATCTCTCAAGATCAACAGCCTGCAG 301

341 CCTGAAGATTTGGGAGTTATTACTGTCAACATTTTGGAGTACTCCGTACAGTTCCGA 400

302 TATGAAGATGTTGGAGTTTATTATGTCTACGGTATGATGATGTTTCCATTCACGTTCCGC 361

401 GGGGGACCAAGTTGGAATAAAACGGGCTGATGTCGACCAACTGTATCTATCTTCCCA 460

362 TCGGGACCAAGTTGGAATAAAACGGGCTGATGTCGACCAACTGTATCTATCTTCCCA 421

461 CCATCACTGAGCAGTTAACATCTCGAGGTGCTCAGTCGCTGCTTCTTGAACAACCTTC 520

422 CCATCACTGAGCAGTTAACATCTCGAGGTGCTCAGTCGCTGCTTCTTGAACAACCTTC 481

521 TACCCCAAGACATCAATGTCAGTGGAGATTTGATGGCAGTGAACGACAAAATGGCGTC 580

QY

482 TACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGGCGTC 541

581 CTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGACACCTTACAGCATGAGCAGCCCTC 640

542 CTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGACACCTTACAGCATGAGCAGCCCTC 601

641 ACGTTGACCAAGACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAG 700

602 ACGTTGACCAAGACGAGTATGAACGACATTAACAGCTATACCTGTGAGGCCACTCACAAG 661

701 ACATCAACTTCAACCATTTCAACAGCTTCAACAGGAATGAGTGTAGAGACAAAGTTC 760

662 ACATCAACTTCAACCATTTCAACAGCTTCAACAGGAATGAGTGTAGAGACAAAGTTC 721

761 TGAGAGCCCAACCCAGTCCCGAGCTCCCAACCTCTCCCTTCTTAAAGTCTTGGAGGC 820

722 TGAGAGCCCAACCCAGTCCCGAGCTCCCGAGCTCCCAACCTCTCCCTTCTTAAAGTCTTGGAGGC 781

821 TTCCCCCAACAGGACCTACCACTGTGGGGTGTCCCAACCTCTCCCTTCTTAAAGTCTTGGAGGC 880

782 TTCCCCCAACAGGACCTACCACTGTGGGGTGTCCCAACCTCTCCCTTCTTAAAGTCTTGGAGGC 841

881 CTCCTCTCCCTTCTTAAAGTCTTGGAGGCCTTATCATGCTATATTTGCAGAAAATATTCATAAAG 940

842 CTCCTCTCCCTTCTTAAAGTCTTGGAGGCCTTATCATGCTATATTTGCAGAAAATATTCATAAAG 901

941 TGAGTCTTTGGCAAAAAAAGAAAAA 970

902 TGAGTCTTTGGCAAAAAAAGAAAAA 931

S65921 998 bp mRNA linear PRI 24-NOV-1993

anti-colorectal carcinoma light chain-glycoprotein CANAG-50

specific IgG1 kappa [human, 19.9 hybridoma, antibody 1116NS19.9,

mRNA, 998 nt].

S65921

S65921.1 GI:425519

Homo sapiens 19.9 hybridoma antibody 1116NS19.9.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 998)

Tongue,D.W., Hennam,J.F., Greene,A.R., Lee,I.D. and Edge,M.D.

Cloning and characterization of 1116NS19.9 heavy and light chain

cDNAs and expression of antibody fragments in Escherichia coli

Year Immunol. 7, 56-62 (1993)

93383497

8372513

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 138017] from the original journal article.

This sequence comes from Fig. 2.

Location/Qualifiers

1..998

/organism="Homo sapiens"

/db_xref="taxon:9606"

1..998

/gene="anti-colorectal carcinoma light chain"

80..790

/gene="anti-colorectal carcinoma light chain"

/note="glycoprotein CANAG-50 specific IgG1 kappa; Method:

conceptual translation with partial peptide sequencing;

This sequence comes from Fig. 2"

/codon_start=1

/product="anti-colorectal carcinoma light chain"

/protein_id="AAB28160.1"

/db_xref="GI:425520"

/translation="MDMTTPAQFLGILLWFFPKIKDKWTQSPSSWYASLGERVTIT

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EDMGYCYCLQYDEFPRTFGGKLEIKRADAAFTVIFPPSSQLTSGGASVVCFLNN

FYPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTLLTKDEYERHNSYTCEA

QY

[illegible][illegible]

Query Match	Score 683.6;	DB 10;	Length 977;
Best Local Similarity	84.9%;	Pred. No. 8e-179;	
Matches 783;	Conservative	0;	Mismatches 124; Indels 15; Gaps 1;
Y	65	CTGGCGTTGCTCTCTCTCTGCTTACAGGTGCCAGATGTGACATCCAGATCACTCAGTCT	124
b	56	CTGTGTGGCTGATGTTCTGGATTCTCTCTCCAGCAGTGATGTGTGATGACCCAAACT	115
Y	125	CCAGCCTCCCTATCTGCGATCTGTGGGAGAACTGTCCACATCATGTCCAGCAAGCTGGG	184
b	116	CCACTCTCCCTGCTGTGCTGAGTCTTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAG	175
Y	185	AATATTCAAAAT-----TATTTTACATGGTATCATCAGCACACACAGGGGAAAA	229
b	176	AGCATTGTACATAGTAAATGGAACACACTATTTAGATGGTACCTTGCAGAACCCAGGCCAG	235
Y	230	TCTCCTCAGCTCCCTGGTCTATTCTGCAAAAACCTTAGTCAGATGTGTGCCATCAAGGTTT	289

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

Run On: June 18, 2003, 16:41:53 ; Search time 33.1938 Seconds
(without alignments)
1452.530 Million cell updates/sec

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Title: US-09-770-916-4
Perfect score: 1234
Sequence: 1 MSUI TQUT NLY TTY TQUT TQUT

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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database :
    SPTREMBL_21:*
    1: sp_archaea.*
    2: sp_bacteria.*
    3: sp_fungi.*
    4: sp_human.*
    5: sp_invertebrate.*
    6: sp_mammal.*
    7: sp_mhc.*
    8: sp_organelle.*
    9: sp_phage.*
    10: sp_plant.*
    11: sp_rodent.*
    12: sp_virus.*
    13: sp_vertebrate.*
    14: sp_unclassified.*
    15: sp_rvirus.*
    16: sp_bacteriap.*
    17: sp_archaeap.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

Result No.	Score	%		Query Match	Length	DB	ID	Description
1	1126	91.2		234	11	Q8VCP0	mus	musculu
2	958	77.6		234	11	Q8R062	mus	musculu
3	946	76.7		233	11	Q91WS9	mus	musculu
4	941	76.3		234	11	Q91WF8	mus	musculu
5	931	75.4		214	11	Q91RIA5	mus	musculu
6	891.5	72.2		238	11	Q95M37	mus	musculu
7	886.5	71.8		238	11	Q8VC16	mus	musculu
8	878	71.2		239	11	Q8VCS5	mus	musculu
9	875.5	70.9		235	11	Q91W12	mus	musculu
10	865	70.1		234	11	Q8R028	mus	musculu
11	668.5	54.2		239	4	Q87CD0	homo	sapien
12	558	45.2		298	11	Q9QYF0	mus	musculu
13	555	45.0		109	11	Q920E6	mus	musculu
14	450	36.5		233	4	Q87BC9	homo	sapien
15	437.5	35.5		237	4	Q8WTU6	homo	sapien
16	436.5	35.4		237	4	Q8WUK4	homo	sapien

17	426.5	34.6	235	11	Q99M11
18	422	34.2	236	4	Q96E61
19	404	32.7	108	4	Q9UL77
20	403	32.5	108	4	Q9UL70
21	400.5	32.5	107	4	Q96SA9
22	395	32.0	240	4	Q8WUK3
23	393.5	31.1	233	4	Q96I69
24	377	30.6	108	4	Q9UL79
25	373.5	30.3	107	4	Q9UL81
26	367	29.7	127	11	Q923S9
27	365	29.6	116	4	Q96PF6
28	360.5	29.2	134	11	Q8VBD0
29	356	28.8	108	4	Q9UL83
30	342.5	27.8	109	4	Q9UL78
31	340.5	27.6	109	4	Q9UL85
32	338	27.4	111	11	Q920E9
33	333	27.0	108	11	Q8VIJ0
34	332.5	26.9	241	11	Q921A6
35	326	26.4	107	11	Q9JL84
36	321.5	26.1	106	5	Q90410
37	319	25.9	107	11	Q9ER29
38	315.5	25.6	109	4	Q9UL86
39	311	25.2	101	11	Q9JL78
40	300	24.3	97	11	Q9JL76
41	291	23.6	103	11	Q9JL90
42	287	23.3	99	11	Q9JL74
43	277	22.4	114	4	Q9UL80
44	275.5	22.3	104	11	Q9JL42
45	269	21.8	109	6	Q9N0W5
					Q99M11 mus musculus
					Q96E61 homo sapien
					Q9UL77 homo sapien
					Q9UL70 homo sapien
					Q96SA9 homo sapien
					Q8WUK3 homo sapien
					Q96I69 homo sapien
					Q9UL79 homo sapien
					Q9UL81 homo sapien
					Q923S9 mus musculus
					Q96PF6 homo sapien
					Q8VBD0 mus musculus
					Q9UL83 homo sapien
					Q9UL78 homo sapien
					Q9UL85 homo sapien
					Q920E9 mus musculus
					Q8VIJ0 mus musculus
					Q921A6 mus musculus
					Q9JL84 mus musculus
					Q90410 schistosoma
					Q9ER29 mus musculus
					Q9UL86 homo sapien
					Q9JL78 mus musculus
					Q9JL76 mus musculus
					Q9JL80 mus musculus
					Q9JL74 mus musculus
					Q9UL80 homo sapien
					Q9JL82 mus musculus
					Q9N0W5 cryctolagus

ALIGNMENTS

[illegible]

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Query Match          91.2%; Score 1126; DB 11; Length 234;
Best Local Similarity 92.7%; Pred. No. 1.7e-94;
Matches 217; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy'
1 MSVLTQVLALLLLWTGARDTOMTQSPASLSASVGETVTITCRASGNITONYLAWYQQTQ 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
db
1 MSVPTQVLGLLLCLLTGARDCIQLTQSPASLSASVGETVTITCRASNIYSYLAWTQQKQ 60
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy
61 GKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCHWFSTPYTFGG 120

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RESULT 5
Q9RIA5 ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RL single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR HSSP; AF152371; AAD40242.1; -.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGV; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT TER 1
FT SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match
Best Local Similarity 75.4%; Score 931; DB 11; Length 214;
Matches 175; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITCRASGNTQNYLAWYQQTQKSPQLLYVSAKTLADGVPS 80
Db 1 DIQLTQSPSMYASLGERVTITCKASQDINSLSWFOQKPGKSPKTLIYRANRLVDGVP 60
QY 81 RPSGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGFKLEIKRADAAPTYSIFPP 140
Db 61 RPSGSGSGDYSLATSSLEYEDMGIVYCLQYDFEFTFGSGFKLEIKRADAAPTYSIFPP 120
QY 141 SSEQLTSGASVCFNNFYKPDINVKWIDGSRONGVLSWTDQDSKDSYSSSLT 200
Db 121 SSEQLTSGASVCFNNFYKPDINVKWIDGSRONGVLSWTDQDSKDSYSSSLT 200
QY 201 LTKDEYERHNSYTCETHKTSPTIVKSFNRNEC 234
Db 181 LTKDEYERHNSYTCETHKTSPTIVKSFNRNEC 214

RESULT 6
Q99M37 Q99M37 PRELIMINARY; PRT; 238 AA.
T C 01-JUN-2001 (Tremblrel. 17, Created)
T C 01-JUN-2001 (Tremblrel. 17, Last sequence update)
T E 01-DEC-2001 (Tremblrel. 19, Last annotation update)
E Hypothetical 26.3 kDa protein.
S Mus musculus (Mouse).
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR HSSP; P01679; 2EBJ.
DR InterPro; IPR003599; Ig.
QY 8 LALLLLWTGARDIQMTQSPASLSASVGETVITCRASGNTQNYLAWYQQTQKSPQLLYVS 62
Db 7 LLVLMFWIPASSSDVVMVTQTPLSLPVSLGDAQSISCRSSQSVHSNGNTYLEWYLQKPGQ 66
QY 63 SPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGT 122

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DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00410; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match
Best Local Similarity 72.2%; Score 891.5; DB 11; Length 238;
Matches 168; Conservative 20; Mismatches 39; Indels 5; Gaps 1;

QY 8 LALLLLWTGARDIQMTQSPASLSASVGETVITCRASGNTQNYLAWYQQTQKSPQLLYVS 62
Db 7 LLVLMFWIPASSSDVVMVTQTPLSLPVSLGDAQSISCRSSQSVHSNGNTYLEWYLQKPGQ 66
QY 63 SPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGT 122
Db 67 SPKLLIYKVSNRFGSDVPMDFRFGSGSGTDTLTKISRVEADLGVIYCFQSGSHVPTFGSGT 126
QY 123 KLEIKRADAAPTYSIFPPSSSGLTSGGASVCFNNFYKPDINVKWIDGSRONGVLS 182
Db 127 KLEIKRADAAPTYSIFPPSSSGLTSGGASVCFNNFYKPDINVKWIDGSRONGVLS 186
QY 183 WTDQDSKDSYSSSLTTLTKDEYERHNSYTCETHKTSPTIVKSFNRNEC 234
Db 187 WTDQDSKDSYSSSLTTLTKDEYERHNSYTCETHKTSPTIVKSFNRNEC 238

RESULT 7
Q8VC16 ID Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match
Best Local Similarity 71.8%; Score 886.5; DB 11; Length 238;
Matches 167; Conservative 20; Mismatches 40; Indels 5; Gaps 1;

QY 8 LALLLLWTGARDIQMTQSPASLSASVGETVITCRASGNTQNYLAWYQQTQKSPQLLYVS 62
Db 7 LLVLMFWIPASSSDVVMVTQTPLSLPVSLGDAQSISCRSSQSVHSNGNTYLEWYLQKPGQ 66
QY 63 SPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGT 122

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[illegible]

Db 181 NSWTDQDSDSTYSMSSTLTITKDEYERHNSYTCETHKSTSPYKSFNRNEC 234

RESULT 11

Q8TCD0
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 54.2%; Score 668.5; DB 4; Length 239;
Best Local Similarity 52.7%; Pred. No. 7.3e-53;
Matches 126; Conservative 39; Mismatches 69; Indels 5; Gaps 1;
QY 1 MSVLTQVLALLLWLTGARCIDIQMTQSPASLSASVGTVTITCRASGNI-----QNYLAW 55
Db 1 MRPLAQLGLLWLVPGSGDVMVTQSLPVLTPGASISCRSTQSLVSDGNTYLNW 60
QY 56 YQQTQKSPOLLVYSAKTLADGVPSPRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPT 115
Db 61 FQRPQSPRLYKVNRSQDGVPPDRFGSGSGTDFTKITRVEAEDGVYFCMQGTHWP 120
QY 116 YTFGGTQKLEIKRADAAPTVFPSPSEQLTSGGASVVCFLNNFYPKDINVKWKDGSR 175
Db 121 STFGQGTQKLEIKRTVAAPSVFFPPDEQLKSGTSASVVCLLNFPYPREAKVQKVDNALQ 180
QY 176 QNGVLNSWTDQDSDKSTYSMSSTLTITKDEYERHNSYTCETHKSTSPYKSFNRNEC 234
Db 181 SGNQSFVTEQDSDKSTYSLSSTLTLSKADYKHKYACEVTHOGLSSPVTKSFNRGEC 239

RESULT 12

Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE CN 8 scfv.
DE CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLLEN;
RC MEDLINE=20183931; PubMed=10706631;
RC Shinohara N., Demura T., Fukuda H.;
RC "Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method."
Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
EMBL; AB036341; BAA88633.1; -
HSSP; P01607; 1REI.
InterPro; IPR003006; Iq_MHC.
InterPro; IPR003596; Iq_V.
Pfam; PF000047; Iq; 2.
SMART; SM00406; IqV; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
Query Match 45.2%; Score 558; DB 11; Length 298;
Best Local Similarity 89.1%; Pred. No. 1.1e-42;
Matches 106; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 17 GARCDIQMTQSPASLSASVGTVTITCRASGNIQNYLAWYQQTQKSPOLLVYSAKTLAD 76
Db 169 GGSGLDIETQSPASLSASVGTVTITCRASGNIHNYLAWYQQTQKSPOLLVYNAKTLAD 228
QY 77 GVPSPRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTTFFGGTQKLEIKRADAAPTV 135
Db 229 GVPSPRFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTTFFGGTQKLEIKRADAAAPV 287

RESULT 13

Q920E6
ID Q920E6 PRELIMINARY; PRT; 109 AA.
AC Q920E6;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -
DR InterPro; IPR003006; Iq_MHC.
DR Pfam; PF000047; Iq; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F9E05DD1501 CRC64;
Query Match 45.0%; Score 555; DB 11; Length 109;
Best Local Similarity 96.3%; Pred. No. 5.1e-43;
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGTVTITCRASGNIQNYLAWYQQTQKSPOLLVYSAKTLADGVPS 80
Db 1 DIQMTQSPASLSASVGTVTITCRASGNIHNYLAWYQQTQKSPOLLVYNAKTLADGVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTTFFGGTQKLEIKRA 129
Db 61 RFGSGSGTQYSLKINSLOPEDFGSYQCQHFWSPTTFFGGTQKLEIKRA 109

RESULT 14

Q8TEC9
ID Q8TEC9 PRELIMINARY; PRT; 233 AA.
AC Q8TEC9;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Hypothetical 24.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022823; AAH22823.1; -
KW Hypothetical protein.

Search completed: June 18, 2003, 16:46:08
Job time : 34.1938 secs

[illegible]

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RESULT 15
8WTU6 PRELIMINARY; PRT; 237 AA.
D Q8WTU6
C Q8WTU6;
T 01-NAR-2002 (TREMBLrel. 20, Created)
T 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
T 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
T 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
S Hypothetical 24.9 kDa protein.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
N SEQUENCE FROM N.A.
C TISSUE=TONSIL;
C SUBMITTED (JAN-2002) to the EMBL/GenBank/DBJ databases.
L EMBL; BC022098; AAH22098.1; -.
R InterPro: IPR003599; Ig.
R InterPro: IPR003597; Ig_c1.
R InterPro: IPR003006; Ig_MHC.
R InterPro: IPR003596; Ig_v.
R Pfam; PF000047; Ig; 2.
R SMART; SM00409; IG; 2.
R SMART; SM00407; IGC1; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;

Query Match 35.5%; Score 437.5; DB 4; Length 237;
Best Local Similarity 42.6%; Pred. No. 7.4e-32;
Matches 100; Conservative 41; Mismatches 83; Indels 11; Gaps 63

7 VLALLLWLTCARDIQMTQSPASLSASVGETVITICR-ASGNI-QNY-LAWYQQTGKGS 63
6 LLTLLTLLAHCTGSGNAQSVLTQ-PPSVSGAPGQQRVTISCTGSSSNIAGDYVHWYQLPGTA 64

64 POLLVYSAKTLADGVPSPRFGSGSGSGTQYSLKINSLOPEDFGSIYCOHF---WSTPYTFGG 120
65 PKLLIYGNNSNPSPGVPDRFSGSKSGTASLAITGLQAEADYICQSYDYSLSASGVFGG 124

121 GTKLEI-KRADAAPTIVSIFPPPSSEQLTSGGASVCFVFNFFPKDINVKWIDGSEKNGV 179
125 GTKTLVLGQPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKAQSSPVKAGV 184

180 LNSWTDQDSKOSTYSMSSTLTFLKDEYERHNSVTCETAKHTKTSPIVKVSFNREC 234
185 -ETTPPSQSNKSYAAASYLSLTPPEQWKSHRSYSCQWTEHGST--VEKIVAPTEC 236

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: June 18, 2003, 16:41:52 ; Search time 9.5309 seconds
(without alignments)
1018.315 Million cell updates/sec

Title:
Perfect score: 1234

Sequence: 1 MSVLTVLALLLLWLTGARC.....EATHKTSTSPVKSFRNEC 234

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	586	47.5	115	1	KV5C_MOUSE
2	565	45.8	106	1	KACA_MOUSE
3	481	39.0	106	1	KACA_RAT
4	481	39.0	108	1	KVSD_MOUSE
5	466	37.8	106	1	KACB_RAT
6	453	36.7	129	1	KV1W_HUMAN
7	436	35.3	129	1	KV1X_HUMAN
8	409	33.1	117	1	KV1J_HUMAN
9	402	32.6	128	1	KV5E_MOUSE
10	401	32.5	108	1	KV1S_HUMAN
11	399	32.3	108	1	KV1H_HUMAN
12	396	32.1	108	1	KV1C_HUMAN
13	395	32.0	108	1	KV1O_HUMAN
14	392	31.8	108	1	KV1V_HUMAN
15	392	31.8	117	1	KV1I_HUMAN
16	388	31.4	108	1	KV1L_HUMAN
17	387	31.4	108	1	KV4C_HUMAN
18	386	31.3	134	1	KV3K_HUMAN
19	384	31.1	128	1	KV1N_HUMAN
20	381	30.9	108	1	KV1E_HUMAN
21	381	30.9	108	1	KV1Y_HUMAN
22	378	30.6	108	1	KV1Z_HUMAN
23	377.5	30.6	129	1	KV3H_HUMAN
24	375.5	30.4	133	1	KV4B_HUMAN
25	375	30.4	108	1	KV1B_HUMAN
26	374.5	30.3	129	1	KV3M_HUMAN
27	374	30.3	108	1	KV1P_HUMAN
28	373.5	30.3	129	1	KV3L_HUMAN
29	372.5	30.2	107	1	KV1D_HUMAN
30	371	30.1	108	1	KV1Q_HUMAN
31	369	29.9	108	1	KV1F_HUMAN
32	367	29.7	108	1	KV1M_HUMAN
33	367	29.7	130	1	KV5G_MOUSE

ALIGNMENTS

RESULT 1

KV5C_MOUSE
ID KV5C_MOUSE STANDARD; PRT: 115 AA.
AC P01635;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region K2 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8015999; PubMed=6767723;
RA Nishiooka Y., Leder P.;
RT "Organization and complete sequence of identical embryonic and
RT plasmacytoma kappa V-region genes.";
RL J. Biol. Chem. 255:3691-3694(1980).
CC -1- MISCELLANEOUS: THE GENE WAS ISOLATED AND SEQUENCED SEPARATELY FROM
CC TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PLASMACYTOMA CELLS
CC THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.
CC
CC
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CC
CC EMBL; V00778; CAA24155.1; -
CC PIR; A01918; KVMK2.
CC HSP; P01607; IREI.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL
CC CHAIN 1 20
CC 21 >115 IG KAPPA CHAIN V-V REGION K2.
CC DOMAIN 21 43 FRAMEWORK-1.
CC DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 69 FRAMEWORK-2.
CC DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 77 108 FRAMEWORK-3.
CC DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING-3.
CC DISULFID 43 108 BY SIMILARITY.
CC NON_TER 115 115
CC SEQUENCE 115 AA; 12581 MW; 4F41E3D40C539DEC CRC64;
Query Match 47.5%; Score 586; DB 1; Length 115;
Best Local Similarity 97.4%; Pred. No. 1.8e-40;
Matches 112; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSVLTVLALLLLWLTGARCIDIQTSPASLSASVGETVTITCRASGNITQNLAWYQQOQ 60

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CC entities requires a license agreement (See [http://www.isb-sib.ch/anne](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; V00807; CAA24189.1; -
CC PIR; A02119; KIMS
CC PIR; S01320; S01320.
CC DR HSSP; P01842; 7FAB.
CC DR MGI; 96495; Igk-C.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003597; Ig_cl.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00407; IGcl; 1.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW Immunoglobulin domain; Immunoglobulin C region.
CC FT NON_TER 1 1
CC FT DISULFID 26 86
CC FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
CC SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49ABE5 CRC64;
CC
Query Match 45.8%; Score 565; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.9e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQNGVLSWTQDS 188
DB 1 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQNGVLSWTQDS 60
QY 189 KDTYSMSSTLTLTCKDEYRHSNTCEATHTKSTSPIVKSFNRNEC 234
DB 61 KDTYSMSSTLTLTCKDEYRHSNTCEATHTKSTSPIVKSFNRNEC 106
RESULT 3
KACA_RAT
ID KACA_RAT STANDARD; PRT; 106 AA.
AC P01836;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain C region, A allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
DR PIR; A02118; KIRTA.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR KW Immunoglobulin domain; Immunoglobulin C region.
CC FT NON_TER 1 1
CC FT DISULFID 26 86
CC FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
CC SQ SEQUENCE 106 AA; 11732 MW; B7EL20D9700DD66 CRC64;
CC
Query Match 39.0%; Score 481; DB 1; Length 106;
Best Local Similarity 84.0%; Pred. No. 4.2e-32;
Matches 89; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 129 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQNGVLSWTQDS 188
DB 1 ADAAPTYSIFPPSSQELTSGGASVVCFLNNFYPRDINVKWKIDGSRQNGVLSWTQDS 60

1 MSVLQVLAALLLWLTGARDIQMTQSPASLSASGETVTITCRASGNHNYLAWTQQKQ 60
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPFDGSGYCYCHFWSTP 115
61 GKSPQLLVYNAKTLADGVPSRFGSGSGTQYSLKINSLOPFDGSGYCYCHFWSTP 115
RESULT 2
AC_MOUSE
D KAC_MOUSE STANDARD; PRT; 106 AA.
C P01837;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 16-OCT-2001 (Rel. 40, Last annotation update)
E Ig kappa chain C region.
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
X NCBI_TaxID=10090;
[1]
N SEQUENCE (MOPC 21).
N MEDLINE=73053310; PubMed=4638343;
A Svasti J., Milstein C.;
T "The complete amino acid sequence of a mouse kappa light chain.";
L Biochem. J. 128:427-444(1972).
[2]
N DISULFIDE BONDS (MOPC 21).
N MEDLINE=73008889; PubMed=5073237;
A Svasti J., Milstein C.;
T "The disulphide bridges of a mouse immunoglobulin G1 protein.";
L Biochem. J. 126:837-850(1972).
[3]
N SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
N MEDLINE=79084137; PubMed=103625;
X Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
T "Complete sequence of constant and 3' noncoding regions of an
T immunoglobulin mRNA using the dideoxynucleotide method of RNA
T sequencing.";
L Cell 15:1067-1075(1978).
[4]
N SEQUENCE FROM N.A.
N MEDLINE=82059477; PubMed=6170937;
X Hamlyn P.H., Gait M.J., Milstein C.;
T "Complete sequence of an immunoglobulin mRNA using specific priming
T and the dideoxynucleotide method of RNA sequencing.";
L Nucleic Acids Res. 9:4485-4494(1981).
[5]
N SEQUENCE FROM N.A.
N MEDLINE=81191915; PubMed=6262318;
X Max E.E., Maizel J.V. Jr., Leder P.;
T "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
T mouse kappa immunoglobulin J and C region genes.";
L J. Biol. Chem. 256:5116-5120(1981).
[6]
N SEQUENCE FROM N.A.
N MEDLINE=81198949; PubMed=6785724;
X Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
T "DNA sequence of the constant gene region of the mouse immunoglobulin
T kappa chain.";
L Nucleic Acids Res. 9:971-981(1981).
[7]
N SEQUENCE FROM N.A.
N MEDLINE=88329081; PubMed=3138116;
X de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
T "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
T directed against the tumour marker human placental alkaline
T phosphatase.";
L Eur. J. Biochem. 176:287-295(1988).

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Db 1 ADAAPTIVSIFPPSMEQLTSGGATVVCVFNFNYPDRISVKWKIDSGEQRDGVLDSTVDQDS 60
QY 189 KDSYSSMSSTLTLPKDEYERHNSYTCETHKTSPIVKSFNRRNC 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 KDSYSSMSSTLTLPKDEYERHNSYTCETHKTSPIVKSFNRRNC 106

RESULT 4
KV5D_MOUSE
ID KV5D_MOUSE STANDARD; PRT; 108 AA.
AC P01636;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MOPC 149.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=82057806; PubMed=6795447;
RA Appella E., Alvarez V.L.;
RT "Amino acid sequence of the variable region of M149 mouse myeloma
RT light chain: comparison with the nucleotide sequence of K2 and K3
RT clones.";
RL Mol. Immunol. 17:1507-1513(1980).
CC -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01919; KWS49.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23
  FT DOMAIN 24 34 FRAMEWORK-1.
  FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
  FT DOMAIN 50 56 FRAMEWORK-2.
  FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
  FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
  FT DOMAIN 98 108 FRAMEWORK-4.
  FT DISULFID 23 88 BY SIMILARITY.
  FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12030 MW; 0B5244D2B410D84C CRC64;

Query Match 39.0%; Score 481; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 4.3e-32;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQKSPQLLYSAKTLADGVPS 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    1 DIQMTQSPDLSASVGETVTITCRASNIYSYLAWYQKQKSPQLLYDAKTLVEGVPS 60

QY 81 RFSGSGGTQYSLKINSLOPEDFGSYCYOHFWSTPTFGGKLEIKR 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    61 RFSGSGGTQYSLKINSLOPEDFGSYCYOHFWSTPTFGGKLEIKR 108

RESULT 5
KACB_RAT
ID KACB_RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=LOU;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes.";
RL J. Immunol. 115:59-62(1975).
DR PIR; A02117; K1RTB.
DR HSP; P01842; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00290; IGMHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
  FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
  FT CONFLICT 106 106 D -> N (IN REF. 2).
  FT CONFLICT 30 30 N -> K (IN REF. 2).
  FT CONFLICT 48 48 MISSING (IN REF. 2).
  FT CONFLICT 79 79 E -> Q (IN REF. 2).
  FT CONFLICT 87 87 E -> Q (IN REF. 2).
  FT CONFLICT 98 98 V -> VW (IN REF. 2).
  FT CONFLICT 100 100 S -> N (IN REF. 2).
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820DICA36 CRC64;

Query Match 37.8%; Score 466; DB 1; Length 106;
Best Local Similarity 80.2%; Pred. No. 6.6e-31;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 129 ADAAPTIVSIFPPSMEQLTSGGATVVCVFNFNYPDRISVKWKIDSGEQRDGVLDSTVDQDS 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    1 ADAAPTIVSIFPPSMEQLTSGGATVVCVFNFNYPDRISVKWKIDSGEQRDGVLDSTVDQDS 60

QY 189 KDSYSSMSSTLTLPKDEYERHNSYTCETHKTSPIVKSFNRRNC 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    61 KDSYSSMSSTLTLPKDEYERHNSYTCETHKTSPIVKSFNRRNC 106
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RESULT 6
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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```

Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
SIGNAL
CHAIN 22
DOMAIN 23 129
DOMAIN 23 45
DOMAIN 46 56
DOMAIN 57 71
DOMAIN 72 78
DOMAIN 79 110
DOMAIN 111 119
DOMAIN 120 129
DISULFID 45 110
NON_TER 129 129
SEQUENCE 129 AA; 14235 MW; CAF076BC7B5574C8 CRC64;
Query Match 35.3%; Score 436; DB 1; Length 129;
Best Local Similarity 64.6%; Pred. No. 2.1e-28; Indels 0; Gaps 0;
Matches 82; Conservative 18; Mismatches 27;
OY 1 MSVLQVQLALLLWLTGARGCDIQMTSPASLSASVGCTVTITCRASGNIONYLAWYQQQTQ 60
DbD 3 MRVPALQLGLLWLRLRRVCDIQMTSPSLSASVGDRVTITCRAGNINIFLSWYQKP 62
OY 61 GKSPOLLVYSAKTLADGVPSRFGSGSGGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGG 120
DbD 63 GKAPLLIYAVSNLQGVPSRFGSGSGAEFTLTISSLOPEDFATYYCCQNYNFSTFFGG 122
OY 121 GTKLEIK 127
DbD 123 GTKVDNK 129
RESULT 8
KVIJ_HUMAN STANDARD; PRT; 117 AA.
ID KVIJ_HUMAN
AC P01602;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK102 precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RT Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene.";
RT Nature 288:730-733(1980).
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CC -----
CC EMBL; J00245; AAA59087.1; -
DR EMBL; Z00001; CAA7292.1; -
DR PIR; A01882; KIHU12.
DR HSSP; P01607; IREI.
DR Genew; HGNC:5741; IGKV1-5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KT SIGNAL 1
FT CHAIN 23 >117
IG KAPPA CHAIN V-I REGION HK102.

FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 >117
FT DISULFID 45 110
FT NON_TER 117 117
SQ SEQUENCE 117 AA; AD1DF3A40AF1A49B CRC64;

Query Match
Best Local Similarity 33.1%; Score 409; DB 1; Length 117;
Matches 75; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSLVTLQVLAALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
DB 3 MRVPAQLLGLLLWLPFGAKCDIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQOKP 62
QY 61 GKSPQLLYVSATKLDGVPFRSGSGSGTQYSLKINSLOPEDFGSGYQCH 111
DB 63 GKAPKLLIYDASSLESVPSRSGSGSGTFTLTISLQPDFFATYQOY 113

RESULT 9
KV5E_MOUSE
ID KV5E_MOUSE STANDARD; PRT: 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma."
RL Nature 287:603-607(1980).
CC -----
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CC -----
CC EMBL: V00772; CAA24150.1; -;
DR PIR: A01920; KYHST1.
DR HSSP: P80362; IWLTL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Igv; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION T1.
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 127
FT DISULFID 43 108
FT NON_TER 128 128
SQ SEQUENCE 128 AA; AFA5563D31BB7E05 CRC64;

Query Match
Best Local Similarity 32.6%; Score 402; DB 1; Length 128;

Best Local Similarity 59.4%; Pred. No. 1.le-25;
Matches 76; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSLVTLQVLAALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
DB 1 MRPQAQFLGLLLWFPFGIKCDIKMTQSPSSVYASLGERTVITCKASQDINSYLTWFQOKP 60
QY 61 GKSPQLLYVSATKLDGVPFRSGSGSGTQYSLKINSLOPEDFGSGYQCHFWSTPTTFGG 120
DB 61 GKSPKTLTYRANRLVDGVPFRSGSGSGQDFTLTISLVEDNGIYCYQYDEPLTFGA 120
QY 121 GTKLEIKR 128
DB 121 GTKLEIKR 128

RESULT 10
KV1S_HUMAN
ID KV1S_HUMAN STANDARD; PRT: 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
high-pressure liquid chromatography. The primary structure of a
monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
Wes)."
RL Hoppe-Sevler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01877; K1HUWS.
DR HSSP: P80362; IWLTL.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Igv; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match
Best Local Similarity 32.5%; Score 401; DB 1; Length 108;
Matches 74; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 21 DIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQCKSPQLLYVSATKLDGVP 80
DB 1 DIOMTQSPSSVSVSGVDRVITTCRASQDISHLAWYQOKSGKAPKLLIYSSASLENGVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSGYQCHFWSTPTTFGGTKLEIKR 128
DB 61 RFGSGSGTFTLTISLQPDFFATYFCQAHSVPLTFGGGTTVDIKR 108

RESULT 11
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT: 108 AA.


```

C P01600;
T 21-JUL-1986 (Rel. 01, Created)
T 21-JUL-1986 (Rel. 01, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
E Ig kappa chain V-I region Hau.
E Homo sapiens (Human).
S Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
X [1]
P MEDLINE=71032830; PubMed=4097974;
X Watanabe S., Hilschmann N.;
A "The primary structure of a monoclonal kappa-type immunoglobulin L-
T chain of subgroup I (Bence-Jones Protein Hau): subdivision within
T subgroups.";
T Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
C -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C PIR; A01868; KIHUBI.
R HSSP; P80362; IWL.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Pfam; PF00047; Ig; 1.
R SMART; SM00406; IgV; 1.
R Immunoglobulin V region; Bence-Jones protein.
X DOMAIN 1 23
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 32.3%; Score 399; DB 1; Length 108;
Best Local Similarity 68.5%; Pred. No. 1.6e-25;
Matches 74; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQKSPOLLVYSAKTLADGVPS 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 DIQMTSPSPSLASVGDRTVITCRASQSDIRNSLIWYQKPGKAPQLIYAASLPSGVPS 60

81 RFSGSGGTQYSLKINSLOPEDFGSYVCOHFWSTPYTFGGGSKLEIKR 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 RFSGSGGTDFLTLSISLQPEDFATYVCOQYNYITPTSGGTRVEIKR 108

RESULT 12
KVIO_HUMAN STANDARD; PRT; 108 AA.
ID KVIO_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Bi.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular their
combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01873; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.

```

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT FT 107 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 958143E1188BCE2A CRC64;
Query Match 32.0%; Score 395; DB 1; Length 108;
Best Local Similarity 69.4%; Pred. No. 3.2e-25;
Matches 75; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
QY 21 DIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQKSPQLLYVSAKTLADGVPS 80
Db 1 DIQMTQSPSLSASVGDRTVITCRASQSDIIKILNWOYTQPKAPKLLIYEASNLQAGVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGKLEIKR 128
Db 61 RFGSGSGTDITFTISSLPEDIATYCYQYQSLPYTFGGGKLIQITR 108
RESULT 14
KVIL_HUMAN STANDARD; PRT; 108 AA.
ID KVIL_HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUEN.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Amyloid.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
Query Match 31.8%; Score 392; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 5.6e-25;
Matches 72; Conservative 17; Mismatches 19; Indels 0; Gaps 0;
QY 21 DIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQKSPQLLYVSAKTLADGVPS 80
Db 1 DIQMTQSPSLSASVGDRTVITCRASQSYVNVANFQOKPKAPKSLIYDASTLOSQVPS 60
QY 81 RFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGGKLEIKR 128
Db 61 NFGSGSGTDITFTISSLPEDIATYCYQYQSLPYTFGGGKLVQIKR 108
RESULT 15
KVIL_HUMAN STANDARD; PRT; 117 AA.
ID KVIL_HUMAN
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
recently duplicated human V kappa sequences have diverged by gene
conversion.";
RL Cell 32:181-189(1983).
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CC -----
DR EMBL; K01322; AAA58930.1; -
DR EMBL; K01324; AAA58932.1; -
DR EMBL; V00556; CAA23824.1; -
DR PIR; A01881; KIHU11.
DR PIR; A21056; A21056.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT FT 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.

Tue Jul 1 18:41:10 2003

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T   DISULFID      45      110
   NON_TER      117
Q   SEQUENCE      117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;
                                     BY SIMILARITY.

Query Match      31.8%; Score 392; DB 1; Length 117;
Best Local Similarity 66.1%; Pred. No. 6.2e-25;
Matches 76; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

y   1 MSVLTQVIALALLLLLTGARCIDIQMTQSPASLSASVGETVITTCRASGNIONIYLAWTQQT 60
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
b   3 MRVLAQLGLLLLLCPGARCIDIQMTQSPSSLSASVGRVITTCRAGOGISSWLAWYQK 62
   . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :

y   61 GKSPOLLVYSAKTLADGVPSRFSGSGGTQYSLKINSIQLPEDFGSYCYQHFNSTP 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
b   63 EKAPKSLIIAASSLQSGVPSPFSGSGGTDFLTLSIQLPEDFAFYCYQQINSTP 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: June 18, 2003, 16:42:32
Job time : 10.5309 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 17.0899 Seconds
(without alignments)
1316.302 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVALLLLWLTGARC.....EATHKTSTPIVKSFNREC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1127	91.3	234	2 S01320	Ig kappa chain pre
2	966	78.3	234	2 S14237	Ig kappa chain pre
3	898	72.8	220	2 A31790	Ig kappa chain pre
4	892.5	72.3	235	2 S25058	Ig kappa chain - m
5	889.5	72.1	225	2 S37484	Ig kappa chain - m
6	887	71.9	214	2 S68212	Ig kappa chain (Ma
7	876	71.0	218	2 JC5810	monoclonal antibod
8	868	70.3	218	2 S68241	Ig kappa chain v r
9	867.5	70.3	219	2 PC4203	Ig kappa chain (mo
10	864.5	70.1	219	2 S52028	Ig kappa chain - m
11	863	69.9	240	2 S06084	Ig kappa chain pre
12	862.5	69.9	219	2 S38865	Ig kappa chain - m
13	860.5	69.7	219	2 S16112	Ig kappa chain v r
14	854.5	69.2	225	2 JL0029	Ig kappa chain pre
15	851.5	69.0	217	2 S42772	Ig kappa chain - m
16	849	68.8	210	2 A56169	Ig kappa chain v r
17	744.5	60.3	230	2 S33161	Ig kappa chain - s
18	704.5	57.1	197	2 S29593	Ig kappa chain (WM
19	689.5	55.9	215	2 JE0244	Ig kappa chain NIG
20	685.5	55.6	215	2 JE0242	Ig kappa chain NIG
21	669.5	54.3	215	2 JE0243	Ig kappa chain NIG
22	642.5	52.1	215	2 A23746	Ig kappa chain V-I
23	639.5	51.8	229	2 A20969	Ig kappa chain pre
24	612	49.6	216	2 JE0241	Ig kappa chain pre
25	592	48.0	128	2 S31488	Ig kappa chain Am3
26	586	47.5	115	1 KWSK2	Ig kappa chain pre
27	579	46.9	134	2 S11245	Ig kappa chain pre
28	578	46.8	178	2 PT0219	Ig kappa chain v-c
29	570	46.2	126	2 I54782	gene Pvt-1a/Ig-Ck

ALIGNMENTS

RESULT 1

S01320

Ig kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000

C:Accession: S01320

R:de Waele, P.; Peys, V.; van de Voorde, A.; Mollemans, F.; Fiers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe

A:Reference number: S01320; MUID:88329081; PMID:3138116

A:Accession: S01320

A:Molecule type: mRNA

A:Residues: 1-234

A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: This sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-234/Product: Ig kappa chain #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match	91.3%	Score	1127;	DB 2;	Length	234;			
Best Local Similarity	91.9%;	Pred. No.	4.6e-63;						
Matches	215;	Conservative	4;	Mismatches	15;	Indels	0;	Gaps	0;
QY	1	MSVLTVALLLLWLTGARC	DIQMTQSPASLSASVGETVITTCRASGNIGNYLAWYQQTQ	60					
Db.	1	MSVPTQVLGILLWLT	DARCDIQMTQSPASLSVSGESVITTCRASNIYSLNLA	YQKQ	60				
QY	61	GKSPQLLVYSAKTLADG	VPFRFSGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG	120					
Db	61	GKSPQLLVYVATKLV	DGVPFRFSGSGSGTQYSLKINSLOPEDFGSYCQHFWDPTPTFGS	120					
QY	121	GTKLETKRADAAPT	VSIFPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE	RQNGVL	180				
Db	121	GTKLEMKRADAAPT	VSIFPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE	RQNGVL	180				
QY	181	NSWTDQDSKSTYSMS	STLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRRNC	234					
Db	181	NSWTDQDSKSTYSMS	STLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRRNC	234					

RESULT 2

S14237

Ig kappa chain precursor (15C5) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S14237

R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Eur. J. Biochem. 192, 767-775, 1990

A:Title: Construction and characterization of a recombinant murine monoclonal antibod

A:Reference number: S14236; MUID:91006173; PMID:2209622

C:Accession: S25058
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
Submitted to the EMBL data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25058
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <FIS>
A:Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 892.5; DB 2; Length 235;
Best Local Similarity 73.3%; Pred. No. 1.5e-48;
Matches 173; Conservative 19; Mismatches 41; Indels 3; Gaps 2;
QY 1 MSVLTVLALLLLWLTG--ARCDIQMTQSPASLSASVGETVTITCRASGNIONYLAWYQQ 58
Db 1 MFOVQIFSLLSIASVILSRGQIVLTQSPAIMSASPEKVTWTCSSASSVSK-MQWYQQ 59
QY 59 TQKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTF 118
Db 60 KSGTSPKRWIYDTSKLASGVPGRFGSGSGTQYSLTSSMEADAATYCCQWSSNPLTF 119
QY 119 GGFTKLEIKRADAAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNG 178
Db 120 GAGTKLEIKRADAAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNG 179
QY 179 VLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234
Db 180 VLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 235

RESULT 5

S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:9406254; PIDN:CAA49869.1; PID:9406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 72.1%; Score 889.5; DB 2; Length 225;
Best Local Similarity 75.9%; Pred. No. 2.1e-48;
Matches 170; Conservative 21; Mismatches 32; Indels 1; Gaps 1;
QY 11 LLLWLTGARCQDIQMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTGSKSPOLLVYS 70
Db 3 LLLCVGANGSIVMTQPKFLLSNGDRVTITCRASQSVNDVAVYQKPGQSPKLLIY 62
QY 71 AKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGTGKLEIKRAD 130
Db 63 ASSRYTGVDPDRFTGSGYCTDFTTISTVQAEADLAVYFCQDYSS-YTFGGGTGKLEIKRAD 121
QY 131 AAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKD 190
Db 122 AAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKD 181
QY 191 STYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234
Db 182 STYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 225

RESULT 6

C:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 78.3%; Score 966; DB 2; Length 234;
Best Local Similarity 77.8%; Pred. No. 4.2e-53;
Matches 182; Conservative 17; Mismatches 35; Indels 0; Gaps 0;
Y 1 MSVLTVLALLLLWLTGARCQDIQMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTQ 60
b 1 MRTPAQFLGLLLWFPGLIKDKMTQSPSSMYASLGSRVTWTCASQDINSYLSWQKP 60
Y 61 GKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFEG 120
b 61 GKSPKTLIYRGNLAVAGVPGRFGSGSGTQYSLTSSLEYEDGVYCYLRYDEFFTFGS 120
Y 121 GTKLEIKRADAAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVL 180
b 121 GTKLEIKRADAAPTIVSIIPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVL 180
Y 181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234
b 181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234

RESULT 3

S31790
g kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
C:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
Biochem. J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:9533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 898; DB 2; Length 220;
Best Local Similarity 76.8%; Pred. No. 6.3e-49;
Matches 169; Conservative 19; Mismatches 26; Indels 6; Gaps 1;
Y 21 DIQMTQSPASLSASVGETVTITCR-----SGNIONYLAWYQQTGSKSPOLLVYSAKTL 74
Db 1 DIVMTQSPSSLTVTAGEKVTMCSQSLNSGKQKYLWYQKPGQPKVLIYWASTR 60
Y 75 ADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGTGKLEIKRADAAPT 134
b 61 ESGVPDRFTGSGSGTDFTLTSSVQAEADLAVYCYNDYSNPLTFGGGTGKLEIKRADAAPT 120
Y 135 VSIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 194
b 121 VSIFPPSSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 180
Y 195 MSSLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234
b 181 MSSLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 220

RESULT 4

S25058
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A: Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A: Reference number: S68211; MUID: 96085223; PMID: 7498516
A: Accession: S68212
A: Status: preliminary; nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-214 <TAK>
A: Cross-references: EMBL:D29668
C: Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 71.9%; Score 887; DB 2; Length 214;
Best Local Similarity 79.0%; Pred. No. 2.9e-48;
Matches 169; Conservative 17; Mismatches 22; Indels 6; Gaps 1;

QY 21 DIQMTQSPASLSASVGETVTITCR-----SGNTQNYLAWYQQTQKSPQLLVYSAKTL 74
Db 1 DIVMTQSPSLAMSVGQKVTWNSCKSSQSLNRSRKNLYAWYQKPGSPKLLVYFASTR 60
QY 75 ADGVPFRSGSGGTQYSLKINSLOPEDFGSYYCOHFWSPTPTFGGGTKLEIKRADAAPT 134
Db 61 ESVGVPDRFISGSGTDFLTITSTVQAEADLADYFCQGHYSTPTFGGGTKLEIKRADAAPT 120
QY 135 VSIFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 194
Db 121 VSIFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 180
QY 195 MSSTLTITKDEYERHNSYTCETHKTSPTIVKS 228
Db 181 MSSTLTITKDEYERHNSYTCETHKTSPTIVKS 214

RESULT 7
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R: Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A: Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A: Reference number: JC5810; MUID: 98063277; PMID: 9398605
A: Accession: JC5810
A: Molecule type: protein
A: Residues: 1-218 <AKA>
C: Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin
C: Superfamily: immunoglobulin V region; immunoglobulin homology
F: 16-94/Domain: immunoglobulin homology <IMM>

Query Match 71.08%; Score 876; DB 2; Length 218;
Best Local Similarity 75.7%; Pred. No. 1.4e-47;
Matches 165; Conservative 20; Mismatches 29; Indels 4; Gaps 1;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNION----YLAWYQQTQKSPQLLVYSAKTLAD 76
Db 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLNLES 60
QY 77 GVPFRSGSGGTQYSLKINSLOPEDFGSYYCOHFWSPTPTFGGGTKLEIKRADAAPT 136
Db 61 GVPFRSGSGGTDFLTINHPVEEDVATYCOHRSRELPFTFGAGTKLEIKRADAAPT 120
QY 137 IFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 196
Db 121 IFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 180
QY 197 STLTITKDEYERHNSYTCETHKTSPTIVKSFNREC 234
Db 181 STLTITKDEYERHNSYTCETHKTSPTIVKSFNREC 218

RESULT 8
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N: Alternate names: immunoglobulin light chain
C: Species: Mus musculus (house mouse)
C: Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C: Accession: S68241; S68214
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL data library, March 1994
A: Description: Specific peroxidase activity by formation of an antibody L chain-porphyrin
A: Reference number: S68241
A: Accession: S68241
A: Molecule type: mRNA
A: Residues: 1-218 <TAK>
A: Cross-references: EMBL:D29670; NID: g473962; PIDN: BAA06141.1; PID: g473963
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A: Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A: Reference number: S68211; MUID: 96085223; PMID: 7498516
A: Accession: S68214
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 'NI', 3-212 <TAK>
A: Cross-references: EMBL:D29670
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: immunoglobulin

Query Match 70.3%; Score 868; DB 2; Length 218;
Best Local Similarity 74.8%; Pred. No. 4.4e-47;
Matches 163; Conservative 21; Mismatches 30; Indels 4; Gaps 1;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNION----YLAWYQQTQKSPQLLVYSAKTLAD 76
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLNLES 60
QY 77 GVPFRSGSGGTQYSLKINSLOPEDFGSYYCOHFWSPTPTFGGGTKLEIKRADAAPT 136
Db 61 GVPFRSGSGGTDFLTINHPVEEDVATYCOHRSRELPFTFGAGTKLEIKRADAAPT 120
QY 137 IFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 196
Db 121 IFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKDSYMS 180
QY 197 STLTITKDEYERHNSYTCETHKTSPTIVKSFNREC 234
Db 181 STLTITKDEYERHNSYTCETHKTSPTIVKSFNREC 218

RESULT 9
PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R: Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A: Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A: Reference number: PC4202; MUID: 97082978; PMID: 8964510
A: Accession: PC4203
A: Molecule type: mRNA
A: Residues: 1-219 <KWA>
A: Cross-references: GB: U29147; NID: g1594225; PIDN: AAC52821.1; PID: g1594226
C: Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C: Superfamily: immunoglobulin V region; immunoglobulin homology
F: 1-112/Domain: V region #status predicted <VRG>
F: 113-219/Domain: C region #status predicted <CRG>

Query Match 70.3%; Score 867.5; DB 2; Length 219;
Best Local Similarity 75.3%; Pred. No. 4.8e-47;
Matches 165; Conservative 16; Mismatches 33; Indels 5; Gaps 1;

21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQQTQKSPQLLVYSAKTLA 75
 1 DVLMTQTPSLPVLGDAISICRSQSIYHTNGNTYLEWYLRKPGQSPKLLIYKVSNR 60
 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTGGGPKLEIKRADAAPT 135
 61 SGVDPDRFGSGSGTDTFLKISRVEAEDLVYCFQGGSHVPTTGGGPKLEIKRADAAPT 120
 136 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195
 121 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180
 196 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 234
 181 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 219

RESULT 10
 S3865
 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C:Accession: S52028
 R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
 submitted to the EMBL Data Library, August 1994
 A:Description: Coordinate expression of antibody subunit genes yields high levels of fun
 A:Reference number: S52028
 A:Status: preliminary
 A:Accession: S52028
 A:Molecule type: mRNA
 A:Residues: 1-219 <V>
 A:Cross-references: EMBL:L35138; NID:9522336; PIDN:AAA67525.1; PID:9522337
 A:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 C:Keywords: immunoglobulin homology <IM>

Query Match 70.1%; Score 864.5; DB 2; Length 219;
 Best Local Similarity 75.3%; Pred. No. 7.3e-47;
 Matches 165; Conservative 15; Mismatches 34; Indels 5; Gaps 1;

21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQQTQKSPQLLVYSAKTLA 75
 1 DVLMTQTPSLPVLGDAISICRSQSIYHTNGNTYLEWYLRKPGQSPKLLIYKVSNR 60
 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTGGGPKLEIKRADAAPT 135
 61 SGVDPDRFGSGSGTDTFLKISRVEAEDLVYCFQGGSHVPTTGGGPKLEIKRADAAPT 120
 136 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195
 121 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180
 196 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 234
 181 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 219

RESULT 11
 S06084
 Ig kappa chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
 C:Accession: S06084
 R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
 Nucleic Acids Res. 17, 7992, 1989
 A:Title: Nucleotide sequence of y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
 A:Reference number: S06084; MUID:90016888; PMID:2508067
 A:Accession: S06084
 A:Molecule type: mRNA
 A:Residues: 1-240 <C>
 A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-240/Product: Ig kappa chain #status predicted <MAT>
 F:153-222/Domain: immunoglobulin homology <IM>

Query Match 69.9%; Score 863; DB 2; Length 240;
 Best Local Similarity 67.5%; Pred. No. 9.9e-47;
 Matches 162; Conservative 31; Mismatches 41; Indels 6; Gaps 1;

Qy 1 MSVLTVQVLAALLMLTGARDIQMTQSPASLSASVGETVITTCRA-----SGNIQNYLA 54
 Db 1 MESQTVQLMSLLWISGTCGDFVMTQSPSSSLAVSAGETVITINCKSSQSLFYSGNKNYLA 60
 55 WYQQTQKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWST 114
 Db 61 WYQQTQKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWST 120
 115 PYTEGGGPKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSE 174
 Db 121 PYTEGGGPKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSE 180
 175 RQGVLSNSWTQDQSKDSTYSMSSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 234
 Db 181 RQGVLSNSWTQDQSKDSTYSMSSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 240

RESULT 12
 S38865
 Ig kappa chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
 C:Accession: S38865
 R:Kipp, B.; Becker, W.; Schlaak, M.
 submitted to the EMBL Data Library, November 1993
 A:Description: Combination of a defined specificity and desired isotype by cloning of
 A:Reference number: S38864
 A:Accession: S38865
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-219 <KIP>
 A:Cross-references: EMBL:227396; NID:9416538; PIDN:CAA81787.1; PID:9416539
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 69.9%; Score 862.5; DB 2; Length 219;
 Best Local Similarity 74.4%; Pred. No. 9.7e-47;
 Matches 163; Conservative 18; Mismatches 33; Indels 5; Gaps 1;

Qy 21 DIQMTQSPASLSASVGETVITTCRASGNI-----QNYLAWYQQTQKSPQLLVYSAKTLA 75
 Db 1 ELVMTQSPSLSVLGDAQSICRSQSIYHTNGNTYLEWYLRKPGQSPKLLIYKVSNR 60
 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTGGGPKLEIKRADAAPT 135
 Db 61 SGVDPDRFGSGSGTDTFLKISRVEAEDLVYCFQGGSHVPTTGGGPKLEIKRADAAPT 120
 136 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 195
 Db 121 SIRPPSSSEQLTSGGASVVCFLNFPKDIINVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180
 196 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 234
 Db 181 SSTLTLTDEYERHNSYTCEATHKTSPIVKSFNREC 219

RESULT 13
 S16112
 Ig kappa chain V region (G2a) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16112
 R:Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D
 Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
 A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp

A:Reference number: S16112; MUID:92000313; PMID:1910583
A:Accession: S16112
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-219 <BIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 860.5; DB 2; Length 219;
Best Local Similarity 74.4%; Pred. No. 1.3e-46;
Matches 163; Conservative 17; Mismatches 34; Indels 5; Gaps 1;
QY 21 DIQMTQSPASLSASVGETVTITCRAS-----GNQNYLAWYQQTQKSPOLLVYSAKTLA 75
DB 1 DVVMTQPLSLPVSILGDAQSISCRSSQSLVHSGNTYLYWLQKPGQSPKLIYRVSNRF 60
QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKLEIKRADAAPT 135
DB 61 SGVDPDRFGSGSGTDFTLKISRVAEDLVYFCQGHVPTFGGTRLEIKRADAAPT 120
QY 136 SIFFPSSQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 195
DB 121 SIFFPSSQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 180
QY 196 SSSLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 234
DB 181 SSSLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 219

RESULT 14
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of Igm and IgG2a antiphospho-
A:Reference number: JL0029; MUID:8811315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <IILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JLR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 69.2%; Score 854.5; DB 2; Length 225;
Best Local Similarity 74.4%; Pred. No. 3.1e-46;
Matches 163; Conservative 15; Mismatches 36; Indels 5; Gaps 1;
QY 21 DIQMTQSPASLSASVGETVTITCRAGNI-----QNYLAWYQQTQKSPOLLVYSAKTLA 75
DB 7 DVLMTQPLSLPVSILGDAQSISCRSSQNIHSTGNTYLYWLQKPGQSPNLIYKISNRF 66
QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKLEIKRADAAPT 135
DB 67 SGVDPDRFGSGSGTDFSLISRVAEDLVYFCQSSHVRWTFGGGKLEIKRADAAPT 126
QY 136 SIFFPSSQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 195
DB 127 SIFFPSSQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 186
QY 196 SSSLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 234
|||||

DB 187 SSSLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 225
RESULT 15
S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
Submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:9414143; PIDN:CAA53226.1; PID:9414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 851.5; DB 2; Length 217;
Best Local Similarity 74.1%; Pred. No. 4.6e-46;
Matches 160; Conservative 18; Mismatches 33; Indels 5; Gaps 1;
QY 24 MTQSPASLSASVGETVTITCRAGNI-----QNYLAWYQQTQKSPOLLVYSAKTLADGV 78
DB 2 MTQSPASLSASVGETVTITCRAGNI-----QNYLAWYQQTQKSPOLLVYSAKTLADGV 61
QY 79 PSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKLEIKRADAAPT 138
DB 62 PSRFGSGSGTDFTLKISRVAEDLVYFCQSHVVRWTFGGGKLEIKRADAAPT 121
QY 139 PPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 198
DB 122 PPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYSTM 181
QY 199 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 234
DB 182 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNNEC 217

Search completed: June 18, 2003, 16:47:05
Job time : 18.0899 secs

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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:57 ; Search time 27.6067 seconds
(without alignments)
2164.388 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLWLTGARC.....EATHKTSPIVKSFNNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1156168 seqs, 255349102 residues

Total number of hits satisfying chosen parameters: 1156168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA.New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	985	79.8	237	6	US-10-219-051B-3411
2	985	79.8	237	6	US-10-219-051B-12786
3	985	79.8	237	6	US-10-219-051B-14374
4	918	74.4	238	6	US-10-384-933-11
5	907	73.5	211	6	US-10-236-051-8
6	881.5	71.4	234	1	PCT-US02-34420A-24
7	881.5	71.4	234	1	PCT-US02-35333A-24
8	881.5	71.4	234	6	US-10-286-132A-24
9	881.5	71.4	234	6	US-10-281-479A-24
10	881.5	71.4	234	6	US-10-275-180A-24
11	881	71.4	236	5	US-09-726-219A-188
12	845	68.5	215	6	US-10-236-051-4
13	830.5	67.3	216	5	US-09-254-180C-132
14	830.5	67.3	216	5	US-09-254-180C-183
15	818.5	66.3	216	5	US-09-254-180C-182
16	806	65.3	234	1	PCT-US02-36107-24
17	806	65.3	234	6	US-10-292-088-24
18	806	65.3	237	1	PCT-US02-22011-109
19	806	65.3	237	6	US-10-194-975-109
20	804	65.2	234	1	PCT-US02-36107-48
21	804	65.2	234	6	US-10-292-088-48
22	804	65.2	241	1	PCT-US03-01096-313
23	803	65.1	236	1	PCT-US03-09260-4
24	803	65.1	236	6	US-10-401-344-4
25	771	62.5	214	5	US-09-618-380A-5
26	766.5	62.1	239	6	US-10-219-051B-12711

27 762 61.8 233 1 PCT-US03-10154-68 Sequence 68, Appl
28 762 61.8 233 6 US-10-404-724-68 Sequence 68, Appl
29 762 61.7 4852 6 US-10-412-406-33 Sequence 33, Appl
30 759 61.5 663 6 US-10-412-406-32 Sequence 32, Appl
31 756.5 61.3 235 6 US-10-405-027-3083 Sequence 3083, Ap
32 756.5 61.3 235 6 US-10-405-027-4346 Sequence 4346, Ap
33 754 61.1 237 1 PCT-US02-27220-4 Sequence 4, Appl
34 754 61.1 237 6 US-10-1227-694-4 Sequence 1, Appl
35 751 60.9 237 1 PCT-US02-27220-1 Sequence 1, Appl
36 751 60.9 237 5 US-09-724-868-10 Sequence 10, Appl
37 751 60.9 237 6 US-10-227-694-1 Sequence 1, Appl
38 751 60.9 237 6 US-10-1234-671-100 Sequence 10, Appl
39 749 60.7 212 1 PCT-US02-40227A-77 Sequence 100, Appl
40 749 60.7 212 6 US-10-320-231A-77 Sequence 77, Appl
41 748 60.6 214 1 PCT-US03-13054-3 Sequence 77, Appl
42 748 60.6 214 6 US-10-423-299-3 Sequence 3, Appl
43 746 60.5 222 6 US-10-424-599-208511 Sequence 3, Appl
44 744 60.3 214 5 US-09-724-868-2 Sequence 208511,
45 744 60.3 214 6 US-10-404-286-11 Sequence 2, Appl
Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-219-051B-3411
; Sequence 3411, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera
; TITLE OF INVENTION: Hospital / Bayer AG
; FILE REFERENCE: Nucleotide sequences involved in pain
; CURRENT APPLICATION NUMBER: US/10219051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3411
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(237)
; OTHER INFORMATION: Xaa-Unknown amino acid
US-10-219-051B-3411

Query Match 79.8% Score 985; DB 6; Length 237;
Best Local Similarity 79.8%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;
QY 1 MSVLTVLALLLWLTGARCIOQTSPASLSASVGTETITCRASGNIONYLAWYQQTQ 60
Db 3 MRPAPFLGILLWFFGCMCDIKWTSPSSWYASLGERVTITCKASODINYSLSWFQKRP 62
QY 61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLOPEDFGSYVQHFWSPTPTFGG 120
Db 63 GKSPKTLIYRANRLVDGVPSRFSGSGSGGQDYSLTISSEYEDMGIIYCLQYDEFPPTFGG 122
QY 121 GYKLEKRAADAPTYSIFPPSSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVL 180
Db 123 GYKLEKRAADAPTYSIFPPSSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVL 182
QY 181 NSWTDDSDSDSYMSSTLTLTDEYERHNSYTCETHKTSSTPIVKSFNNEC 234
Db 183 NSWTDDSDSDSYMSSTLTLTDEYERHNSYTCETHKTSSTPIVKSFNNEC 236

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RESULT 2
US-10-219-051B-12786
Sequence 12786, Application US/10219051B
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 12786
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(237)
OTHER INFORMATION: Xaa=Unknown amino acid
US-10-219-051B-12786

Query Match          79.8%; Score 985; DB 6; Length 237;
Best Local Similarity 79.5%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLWLTGACDIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
3 MRTPAQLGILLWFPKMKDKIMTQSPSSMYASLGERTVITCKASQDINSYLSWFOQKP 62
61 GKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 120
63 GKSPKTLIYRANRLVDGVPSRFGSGSGQDYSLTISSEYEDMGIIYCLQYDEPPTFGG 122
121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180
123 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 182
181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
183 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(237)
OTHER INFORMATION: Xaa=Unknown amino acid

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```

US-10-219-051B-14374
Sequence 14374, Application US/10219051B
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: Lea 35693 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SEQ ID NO 14374
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

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; LOCATION: (1)..(237)
; OTHER INFORMATION: Xaa=Unknown amino acid
US-10-219-051B-14374

Query Match          79.8%; Score 985; DB 6; Length 237;
Best Local Similarity 79.5%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLWLTGACDIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTQ 60
3 MRTPAQLGILLWFPKMKDKIMTQSPSSMYASLGERTVITCKASQDINSYLSWFOQKP 62
61 GKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 120
63 GKSPKTLIYRANRLVDGVPSRFGSGSGQDYSLTISSEYEDMGIIYCLQYDEPPTFGG 122
121 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 180
123 GTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVL 182
181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
183 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236

```

```

RESULT 4
US-10-384-933-11
Sequence 11, Application US/10384933
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
LENGTH: 238
TYPE: PRT
ORGANISM: Mus musculus
US-10-384-933-11

```

```

Query Match          74.4%; Score 918; DB 6; Length 238;
Best Local Similarity 72.3%; Pred. No. 1.7e-72;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

1 MSVLTQVLAALLLLWLTGACDIOMTQSPASLSASVGETVITTCRASGNIONYLAWY 56
1 METDTILLWVWMLWIPGSTGDIIVLTQSPASLAVSGQRATISCKASQSDVDGDSYMWY 60
57 QOTGKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPT 116
61 QOKPGQPPKLLIYAASNLESGIPARFSGSGTDTFLNHPVEEEDATYYCQSNEDPR 120
117 TFGGKTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQ 176
121 TFGGKTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQ 180
177 NGVLSNWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
181 NGVLSNWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238

```

```

RESULT 5
US-10-236-051-8
; Sequence 8, Application US/10236051

```

```
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier J.
; APPLICANT: MORIARTY, Ann M.
; APPLICANT: ULEVITCH, Richard J.
; APPLICANT: TOBIAS, Peter S.
; APPLICANT: MATHISON, John C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP1140-4
; CURRENT APPLICATION NUMBER: US/10/236,051
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/170,769
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/373,297
; PRIOR FILING DATE: 1995-01-23
; PRIOR APPLICATION NUMBER: PCT/US94/05898
; PRIOR FILING DATE: 1994-05-27
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Murine
; US-10-236-051-8

Query Match 73.5%; Score 907; DB 6; Length 211;
Best Local Similarity 81.0%; Pred. No. 1.4e-71;
Matches 171; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 24 MTQSPASLSASVGTVTITCRASGNIGNYLAWYQOTGKSPQLLYVSAKTLADGVPSPRS 83
DB 1 MTQSPSSLSASLGRVITCRASQDINKYLNWYQGGVTKVLYITSLRHSGVPSRFS 60
QY 84 GSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGGTKLEIKRADAAPTVSIFPPSS 143
DB 61 GSGSGTYSLTISNLEQEDFATYFCQGRDLPTWTFGGTKLEIKRADAAPTVSIFPPSS 120
QY 144 QLTSGGASVVCFLNNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLTITK 203
DB 121 QLTSGGASVVCFLNNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLTITK 180
QY 204 DEYERHNSYTCETHKTSPIVKSFNREC 234
DB 181 DEYERHNSYTCETHKTSPIVKSFNREC 211

RESULT 6
PCT-US02-34420A-24
; Sequence 24, Application PC/TUS0234420A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACTOR-
; FILE REFERENCE: 21085.0029P3
; CURRENT APPLICATION NUMBER: PCT/US02/34420A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02

Query Match 71.4%; Score 881.5; DB 1; Length 234;
Best Local Similarity 73.4%; Pred. No. 2.7e-69;
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

QY 2 SVLTQVLALLLLWLTGARCIDIQMTQSPASLSASVGTVTITCRASGNIGNYLAWYQOTG 61
DB 3 SLVLYVYTHYLFAGVEGDIVMTQSHKFMSTSVGDRVSTCKASQDVGTAVAWYQKPG 62
QY 62 KSPQLLYVSAKTLADGVPSPRSFGSGGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGG 121
DB 63 QSPKLLIYWASTRTGTGVPDRFTFGSGGDTFTLTISNVOSELDADYFCQY-SYRTFGG 121
QY 122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRQNGVLN 181
DB 122 TKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRQNGVLN 181
QY* 182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234
DB 182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 7
PCT-US02-35333A-24
; Sequence 24, Application PC/TUS0235333A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; FILE REFERENCE: 21085.0029P2
; CURRENT APPLICATION NUMBER: PCT/US02/35333A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
PCT-US02-35333A-24

Query Match 71.4%; Score 881.5; DB 1; Length 234;
Best Local Similarity 73.4%; Pred. No. 2.7e-69;
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

QY 2 SVLTQVLALLLLWLTGARCIDIQMTQSPASLSASVGTVTITCRASGNIGNYLAWYQOTG 61
DB 3 SLVLYVYTHYLFAGVEGDIVMTQSHKFMSTSVGDRVSTCKASQDVGTAVAWYQKPG 62
QY 62 KSPQLLYVSAKTLADGVPSPRSFGSGGTQYSLKINSLOPEDFGSYCYQHFWSTPYTFGG 121
DB 63 QSPKLLIYWASTRTGTGVPDRFTFGSGGDTFTLTISNVOSELDADYFCQY-SYRTFGG 121
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Db 63 QSPKLLIYWASTRHGTGVPDRFTSGSGTDFLTITSNVQSEDADYFCQY-SSYRTFGG 121
Qy 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Db 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Qy 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234
Db 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 8

US-10-286-132A-24
; Sequence 24, Application US/10286132A
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lofuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286.132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346.402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201.344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
US-10-286-132A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;
Best Local Similarity 73.4%; Pred. No. 2.7e-69;
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;

Qy 2 SVLTQVALLLWLTGARCIDQMTQSPASLSASVGETVITICRASNIGNIYLAWYQQTQ 61
Db 3 SLVLYVYTHYLFLEAGVEGDIVMTQSHKFMSTVSGDRVSITCKASQDVCTAVAWYQKPG 62
Qy 62 KSPQLLYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 121
Db 63 QSPKLLIYWASTRHGTGVPDRFTSGSGTDFLTITSNVQSEDADYFCQY-SSYRTFGG 121
Qy 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Db 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Qy 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234
Db 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 9

US-10-281-479A-24
; Sequence 24, Application US/10281479A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: Lofuglio, Albert S.

; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.002906
; CURRENT APPLICATION NUMBER: US/10/281.479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391.478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346.402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201.344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
US-10-281-479A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;
Best Local Similarity 73.4%; Pred. No. 2.7e-69;
Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;
Qy 2 SVLTQVALLLWLTGARCIDQMTQSPASLSASVGETVITICRASNIGNIYLAWYQQTQ 61
Db 3 SLVLYVYTHYLFLEAGVEGDIVMTQSHKFMSTVSGDRVSITCKASQDVCTAVAWYQKPG 62
Qy 62 KSPQLLYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGG 121
Db 63 QSPKLLIYWASTRHGTGVPDRFTSGSGTDFLTITSNVQSEDADYFCQY-SSYRTFGG 121
Qy 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Db 122 TKLETKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLN 181
Qy 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234
Db 182 SWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234

RESULT 10

US-10-275-180A-24
; Sequence 24, Application US/10275180A
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APO
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275.180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-24

Query Match 71.4%; Score 881.5; DB 6; Length 234;
Best Local Similarity 73.4%; Pred. No. 2.7e-69;

Matches 171; Conservative 20; Mismatches 41; Indels 1; Gaps 1;
QY 2 SVLTQVLAALLMLTGCARDIOMTQSPASLSASVGETVTITCRASGNIONYLAWYQOTQG 61
Db 3 SLVLYVTHYFLFAGVGDIVMTQSHKFMSTSVGDRVSIITCKASQDVGTAVAWYQKRG 62
QY 62 KSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 121
Db 63 QSPKLLIYWASTHTGTVDRFTGSGSGTDFLTISNVQSEDLADYFCQY-SSYRTFGG 121
QY 122 TKLEIKRADAAPTYSIRPPSSSEQLTSGGASVVCFLNNFPKDIWKIDGSRONGVLN 181
Db 122 TKLEIKRADAAPTYSIRPPSSSEQLTSGGASVVCFLNNFPKDIWKIDGSRONGVLN 181
QY 182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSNRNEC 234
Db 182 SWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSNRNEC 234

RESULT 11
US-09-726-219A-188
; Sequence 188, Application US/09726219A
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726.219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971.857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of Fab D1.3 from genetically engineered anti-hen egg-white lys
US-09-726-219A-188

Query Match 71.4%; Score 881; DB 5; Length 236;
Best Local Similarity 73.8%; Pred. No. 3e-69;

Matches 169; Conservative 17; Mismatches 43; Indels 0; Gaps 0;
QY 5 TOVLALLLWLTGARCIDIOMTQSPASLSASVGETVTITCRASGNIONYLAWYQOTQGKSP 64
Db 7 TAAAGLLLLAOPAMADIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQOKGKSP 66
QY 65 QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 124
Db 67 QLLVYTTTTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGG 126
QY 125 ETKRADAAPTYSIRPPSSSEQLTSGGASVVCFLNNFPKDIWKIDGSRONGVLN 184
Db 127 ETKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFPYPRKQVQKVDNALQSGNSQES 186
QY 185 DQDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSNRNEC 233
Db 187 EODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 12
US-10-236-051-4
; Sequence 4, Application US/10236051
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier J.
; APPLICANT: MORIARTY, Ann M.
; APPLICANT: ULEVITCH, Richard J.
; APPLICANT: TOBIAS, Peter S.
; APPLICANT: MATHISON, John C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT
; FILE REFERENCE: SCRIPI140-4
; CURRENT APPLICATION NUMBER: US/10/236,051
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/170,769
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/373,297
; PRIOR FILING DATE: 1995-01-23
; PRIOR APPLICATION NUMBER: PCT/US94/05898
; PRIOR FILING DATE: 1994-05-27
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Murine
US-10-236-051-4

Query Match 68.5%; Score 845; DB 6; Length 215;
Best Local Similarity 74.9%; Pred. No. 3.9e-66;
Matches 161; Conservative 17; Mismatches 33; Indels 4; Gaps 1;
QY 24 MTQSPASLSASVGETVTITCRASGNIONY----LAWYQOTQOGKSPQLLVYSAKTLADGVP 79
Db 1 MTQSPASLSAVSLGORAPYPCRAESVDVSNFHWYQKPGPKLLITYRASNLQSGIP 60
QY 80 SRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSPTPTFGGKLEIKRADAAPTYSIFP 139
Db 61 ARFGSGSRDTFTLTINPVEADVAITYCQSNEDPTTSGGGTLEIKRADAAPLVSIFF 120
QY 140 PSSEQLTSGGASVVCFLNNFPKDIWKIDGSRONGVLN 199
Db 121 PSSEQLTSGGASVVCFLNNFPKDIWKIDYSEKQVNSWTDQDQSKDSTYSMSSTL 180
QY 200 TLTKDEYERHNSYTCEATHKTSTSPIVKSNRNEC 234
Db 181 TLTKDEYERHNSYTCEATHKTSTSPIVKSNRNEC 215

RESULT 13
US-09-254-180C-132
; Sequence 132, Application US/09254180C


```

; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match      67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----ONYLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQPKLLIYKVSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQGSHPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

RESULT 15
US-09-254-180C-182
; Sequence 182, Application US/09254180C
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-254-180C-182

Query Match      66.3%; Score 818.5; DB 5; Length 216;
Best Local Similarity 72.2%; Pred. No. 8.2e-64;
Matches 156; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----YLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQSPOLLVYSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQSNYLPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match      67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----ONYLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQPKLLIYKVSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQGSHPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Mouse
US-09-254-180C-132

Query Match      67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----ONYLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQPKLLIYKVSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQGSHPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match      66.3%; Score 818.5; DB 5; Length 216;
Best Local Similarity 72.2%; Pred. No. 8.2e-64;
Matches 156; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----YLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQSPOLLVYSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQSNYLPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Mus musculus
US-09-254-180C-182

Query Match      66.3%; Score 818.5; DB 5; Length 216;
Best Local Similarity 72.2%; Pred. No. 8.2e-64;
Matches 156; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----YLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQSPOLLVYSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQSNYLPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match      67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----ONYLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQPKLLIYKVSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQGSHPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Mouse
US-09-254-180C-132

Query Match      67.3%; Score 830.5; DB 5; Length 216;
Best Local Similarity 73.1%; Pred. No. 7.3e-65;
Matches 158; Conservative 18; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----ONYLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQPKLLIYKVSNR 60

QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQGSHPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM: Homo sapiens
US-09-254-180C-183

Query Match      66.3%; Score 818.5; DB 5; Length 216;
Best Local Similarity 72.2%; Pred. No. 8.2e-64;
Matches 156; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNI-----YLAWYQQTQKSPOLLVYSAKTLA 75
Db 1 DVLMTQTPLSLPSLGDAQASISCKSSQSIHVSSGNTYFEWYLQKPGQSPOLLVYSNR 60

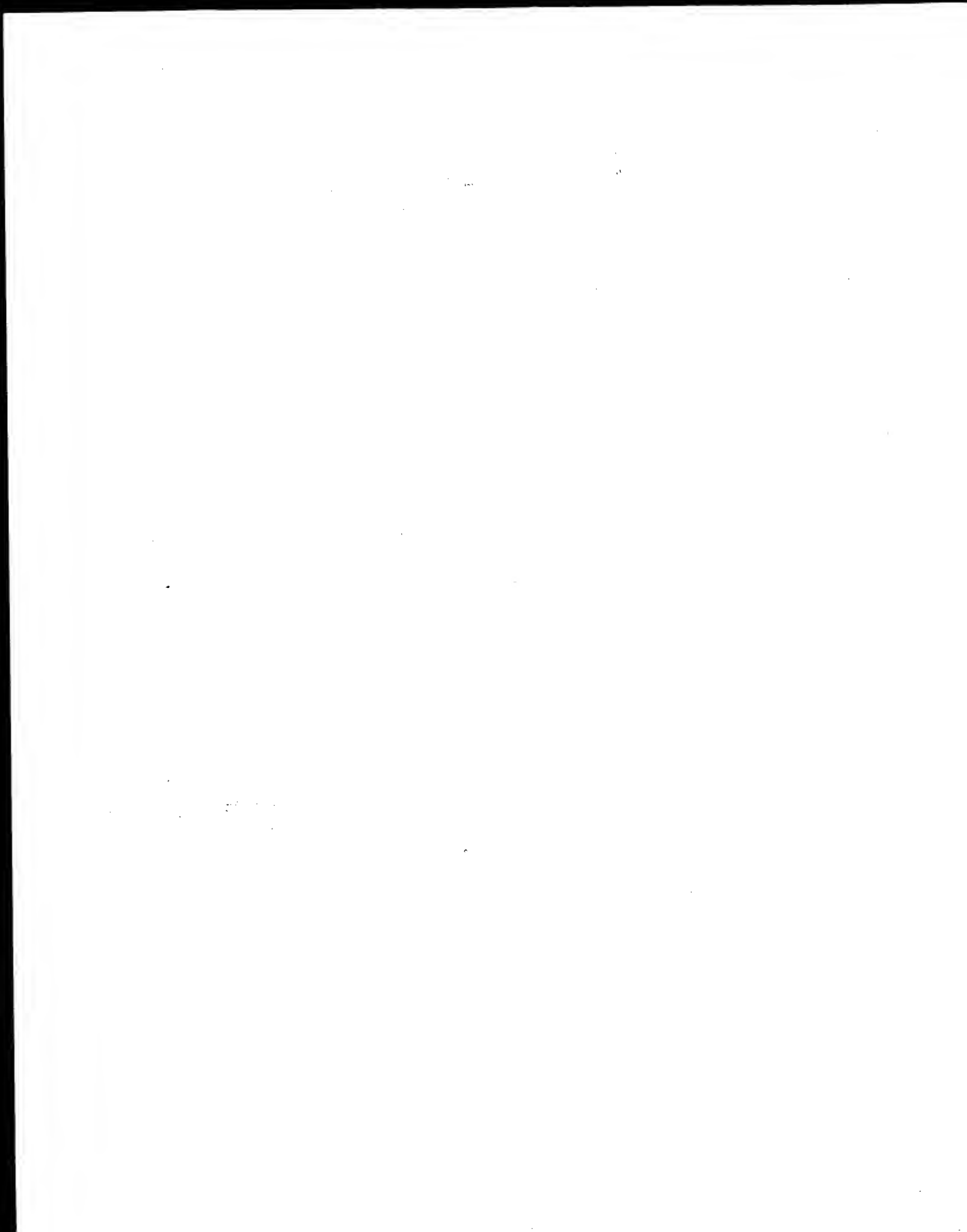
QY 76 DGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFWSPTPTFGGKTLEIKRADAAPT 135
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGVYFCQSNYLPFTFGSGTKLEIKRADAAPT 120

QY 136 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 195
Db 121 SIFFPSSSEQLTSGGASVVCFLNNFYPKIDNWKIDGSRONGVLSNWTDDQSKDSTYS 180

QY 196 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 231
Db 181 SSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFN 216

; ORGANISM
```

Search completed: June 18, 2003, 16:48:37
Job time : 28.6067 secs



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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:44:27 ; Search time 144.935 seconds
(without alignments)
1040.930 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLLWLTGARC.....EATHKSTSPVKSFRNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA.Main.*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
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- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	100.0	234	21	US-09-770-916-4
2	1200	97.2	234	4	US-08-090-534-4
3	1165	94.4	228	21	US-09-791-537-58997
4	1146	92.9	228	21	US-09-791-537-58987
5	1127	91.3	234	21	US-09-791-537-127535
6	1116	90.4	214	21	US-09-791-537-104541

7	1099	89.1	214	21	US-09-791-537-44562
8	1092	88.5	214	21	US-09-791-537-13851
9	1075	87.1	214	21	US-09-791-537-138889
10	1057	85.7	214	21	US-09-791-537-97993
11	1029	83.4	213	21	US-09-791-537-105122
12	985	79.8	236	21	US-09-791-537-89134
13	974.5	79.0	235	21	US-09-791-537-11644
14	970	78.6	234	8	US-08-1480-120-4
15	967	78.4	234	21	US-09-791-537-128696
16	966	78.3	234	21	US-09-791-537-55632
17	947	76.7	214	21	US-09-791-537-110636
18	940	76.2	214	21	US-09-791-537-87447
19	935	75.8	243	21	US-09-791-537-123349
20	933	75.6	214	21	US-09-791-537-88649
21	932	75.5	214	21	US-09-791-537-93651
22	931	75.4	214	21	US-09-791-537-29765
23	930	75.4	243	21	US-09-791-537-74441
24	925	75.0	214	21	US-09-791-537-52722
25	925	75.0	238	20	US-09-613-017-4
26	925	75.0	238	23	US-09-903-327A-4
27	920.5	74.6	213	21	US-09-791-537-27173
28	919.5	74.5	237	21	US-09-791-537-81230
29	918.5	74.4	237	21	US-09-791-537-51510
30	918	74.4	238	14	US-09-053-583-11
31	918	74.4	238	18	US-09-408-646-11
32	918	74.4	238	18	US-09-499-662-11
33	918	74.4	238	26	US-10-216-484-11
34	916	74.2	214	21	US-09-791-537-89445
35	915	74.1	220	21	US-09-791-537-14484
36	914	74.1	214	21	US-09-791-537-138888
37	914	74.1	216	10	US-08-665-839A-40
38	914	74.1	216	10	US-08-665-839B-40
39	910	73.7	212	21	US-09-791-537-107650
40	910	73.7	234	21	US-09-791-537-74535
41	909.5	73.7	235	3	US-07-904-074A-2
42	909	73.7	214	21	US-09-791-537-66254
43	909	73.7	214	21	US-09-791-537-73158
44	909	73.7	214	21	US-09-791-537-85310
45	909	73.7	218	21	US-09-791-537-32984

ALIGNMENTS

RESULT 1

US-09-770-916-4
; Sequence 4, Application US/09770916
; GENERAL INFORMATION:
; APPLICANT: Frank, Dara W.
; APPLICANT: Wiener-Kronish, Jeannine
; APPLICANT: Yahr, Timothy L.
; APPLICANT: Sawa, Teiji
; APPLICANT: Fritz, Robert B.
; TITLE OF INVENTION: Method of and compositions for immunization with the
; FILE REFERENCE: 650053.91487
; CURRENT APPLICATION NUMBER: US/09/770,916
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/448,339
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/109,952
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/126,794
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: mouse
US-09-770-916-4

Query Match

100.0%; Score 1234; DB 21; Length 234;

Best Local Similarity 100.0%; Pred. No. 5.7e-100;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLLTGARDIQMTQSPASLSASVGETVITTCRASNIQNYLAWYQQTQ 60
1 MSVLTQVLAALLLLLTGARDIQMTQSPASLSASVGETVITTCRASNIQNYLAWYQQTQ 60
61 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120
61 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120
121 GTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVL 180
121 GTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVL 180
181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 2

Sequence 4, Application US/08090534
GENERAL INFORMATION:
APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
TITLE OF INVENTION: Disorders in Man
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,534
FILING DATE: 19930719
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: SBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5015
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-090-534-4

Query Match 97.2%; Score 1200; DB 4; Length 234;
Best Local Similarity 97.0%; Pred. No. 5.7e-97;
Matches 227; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

1 MSVLTQVLAALLLLLTGARDIQMTQSPASLSASVGETVITTCRASNIQNYLAWYQQTQ 60
1 MSVLTQVLAALLLLLTGARDIQMTQSPASLSASVGETVITTCRASNIHNYLTWYQKQ 60

Qy 61 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120
Db 61 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGG 120
Qy 121 GTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVL 180
Db 121 GTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVL 180
Qy 181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
Db 181 NSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 3

US-09-791-537-58997
Sequence 58997, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomimix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 58997
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-58997

Query Match 94.4%; Score 1165; DB 21; Length 228;
Best Local Similarity 95.6%; Pred. No. 6.6e-94;
Matches 218; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 7 VLALLLLWLTGARDIQMTQSPASLSASVGETVITTCRASNIQNYLAWYQQTQKSKPOL 66
Db 1 VLGLLLWLTGVRCDIQMTQSPASLSASVGETVITTCRASNIHNYLTWYQKQKSKPOL 60
Qy 67 LVYSAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGSYCQHFWSPTPTFGGSKTLEI 126
Db 61 LVYNAKTLADGVPFRSGSGSGTQYSLKINSIQPEDFGTYYCHHFWSPPTPTFGGSKTLEI 120
Qy 127 KRADAAPTIVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVLSWTQ 186
Db 121 KRADAAPTIVSIFFPSSEQLTSGGASVVCFLNNFYPKIDINVAKWIDGSRQNGVLSWTQ 180
Qy 187 DSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
Db 181 DSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 228

RESULT 4

US-09-791-537-58987
Sequence 58987, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomimix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 58987
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-58987

```
Query Match          92.9%; Score 1146; DB 21; Length 228;
Best Local Similarity 94.3%; Pred. No. 3.1e-92;
Matches 215; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 7 VLALLLWLTGARCDDIOMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQL 66
DB 1 VLGLLLWLTGVRCDIOMTQSPASLSAFVGETVTITCRASGNIHNYLAWYQKQKSPRV 60
QY 67 LVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEI 126
DB 61 LVYAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEI 120
QY 127 KRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQ 186
DB 121 KRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQ 180
QY 187 DSKDYSMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 234
DB 181 DSKDYSMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 228

RESULT 5
US-09-791-537-127535
; Sequence 127535, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 127535
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-127535

Query Match          91.3%; Score 1127; DB 21; Length 234;
Best Local Similarity 91.9%; Pred. No. 1.5e-90;
Matches 215; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 MSVLTQVLLALLLWLTGARCDDIOMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQ 60
DB 1 MSVPTQVLLGLLLWLTGARCDDIOMTQSPASLSVSGESVTITCRASENIYSNLAWYQKQ 60
QY 61 GKSPOLLVYSAKTLADGVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120
DB 61 GKSPOLLVYVATKLVGDVPSRFGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120
QY 121 GPKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVYL 180
DB 121 GPKLEMKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVYL 180
QY 181 NSWTQDQSKDYSMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 234
DB 181 NSWTQDQSKDYSMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 234

RESULT 6
US-09-791-537-104541
; Sequence 104541, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
```

```
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 104541
; LENGTH: 214
; TYPE: PRT
; ORGANISM: pdb 1WEJL
US-09-791-537-104541

Query Match          90.4%; Score 1116; DB 21; Length 214;
Best Local Similarity 98.1%; Pred. No. 1.3e-89;
Matches 210; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQLLVYSAKTLADGVPS 80
DB 1 DIOMTQSPASLSASVGETVTITCRASGNIHNYLAWYQKQKSPQLLVYNKTLADGVPS 60
QY 81 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEIKRADAAPTYSIFPP 140
DB 61 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEIKRADAAPTYSIFPP 120
QY 141 SSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQSKDYSMSSTLT 200
DB 121 SSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQSKDYSMSSTLT 180
QY 201 LTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 234
DB 181 LTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 214

RESULT 7
US-09-791-537-44562
; Sequence 44562, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 44562
; LENGTH: 214
; TYPE: PRT
; ORGANISM: pdb 1FDLL
US-09-791-537-44562

Query Match          89.1%; Score 1099; DB 21; Length 214;
Best Local Similarity 97.2%; Pred. No. 3.9e-88;
Matches 208; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 21 DIOMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTGKSPQLLVYSAKTLADGVPS 80
DB 1 DIOMTQSPASLSASVGETVTITCRASGNIHNYLAWYQKQKSPQLLVYVTTTLADGVPS 60
QY 81 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEIKRADAAPTYSIFPP 140
DB 61 RFGSGSGGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGGTKEIKRADAAPTYSIFPP 120
QY 141 SSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQSKDYSMSSTLT 200
DB 121 SSEQLTSGGASVVCFLNNFYPKIDINVKKIDGSEONGVLSNWDQSKDYSMSSTLT 180
QY 201 LTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 234
DB 181 LTKDEYERHNSYTCEATHKTSTSPIVKSFNREC 214
```

RESULT 8

US-09-791-537-13851
Sequence 13851, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13851
LENGTH: 214
TYPE: PRT
ORGANISM: pdb 1CICC
US-09-791-537-13851

Query Match 88.5%; Score 1092; DB 21; Length 214;
Best Local Similarity 96.3%; Pred. No. 1.6e-87;
Matches 206; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

21 DIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTGCKSPQLLYVYSAKTLADGVPS 80
|||||
1 DIOMTQSPASLSASVGETVITTCRASGNIIHNYLAWYQKQKSPQLLYVYTTTLADGVPS 60
|||||
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 140
|||||
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 120
|||||
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200
|||||
121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180
|||||
201 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
|||||
181 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 214
|||||

RESULT 9
US-09-791-537-138889
Sequence 13889, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13889
LENGTH: 214
TYPE: PRT
ORGANISM: pdb 1KB5L
US-09-791-537-138889

Query Match 87.1%; Score 1075; DB 21; Length 214;
Best Local Similarity 94.9%; Pred. No. 5.1e-86;
Matches 203; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

21 DIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTGCKSPQLLYVYSAKTLADGVPS 80
|||||
1 DIOMTQSPASLSASVGETVITTCRASKNISYLAWYQKQKSPQLLYVYNAKTLGEGVPS 60
|||||
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 140
|||||
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 120
|||||
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200
|||||

Db 121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180
|||||
Qy 201 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
|||||
Db 181 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 214
|||||

RESULT 10

US-09-791-537-97993
Sequence 97993, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 97993
LENGTH: 214
TYPE: PRT
ORGANISM: Mus sp
US-09-791-537-97993

Query Match 85.7%; Score 1057; DB 21; Length 214;
Best Local Similarity 93.0%; Pred. No. 2e-84; 7; Indels 0; Gaps 0;
Matches 199; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

21 DIOMTQSPASLSASVGETVITTCRASGNIONYLAWYQQTGCKSPQLLYVYSAKTLADGVPS 80
|||||
1 ELQMTQSPASLSASVGETVITTCRASNIYSLAWYQKQKSPQLLYVYNAKTLAEGVPS 60
|||||
81 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 140
|||||
61 RFGSGSGTQYSLKINSLOPEDFGSYCQHFWSPTPTFGGCTKLEIKRADAAAPTIVSIFPP 120
|||||
141 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 200
|||||
121 SSELTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLT 180
|||||
Qy 201 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234
|||||
Db 181 LTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 214
|||||

RESULT 11

US-09-791-537-105122
Sequence 105122, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 105122
LENGTH: 213
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-105122

Query Match 83.4%; Score 1029; DB 21; Length 213;
Best Local Similarity 90.6%; Pred. No. 5.7e-82;
Matches 193; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITCRASGNIONYLAWYQOQTQKSPQLLVYSAKTLADGVP 80
 DB 1 DIQMTQSPASLSASVGETVITCRASGNIONYLAWYQOQTQKSPQLLVYNAKDLAEGVPS 60
 QY 81 RFGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTTFFGGTKLETKRADAAPTYSIFPP 140
 DB 61 RFGSGAGTQSLRINSLOPEDFGSYCYQHFWSTPTTFFGGTKLETKRADAAPTYSIFPP 120
 QY 141 SSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVLSNWTQDQSKDSTYSMSSTLT 200
 DB 121 SSQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVLSNWTQDQSKDSTYSMSSTLT 180
 QY 201 LKDEYERHNSYTCEATHKTSPIVKSFNNE 233
 DB 181 LKDEYERHNSYTCEATHKTSPIVKSFNNE 213

RESULT 12
 US-09-791-537-89134
 ; Sequence 89134, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 89134
 ; LENGTH: 236
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-89134

Query Match 79.8%; Score 985; DB 21; Length 236;
 Best Local Similarity 79.5%; Pred. No. 4.9e-78;
 Matches 186; Conservative 16; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSVLTQVALLLLWLTGARCIDQMTQSPASLSASVGETVITCRASGNIONYLAWYQOQTQ 60
 DB 3 MRPQAQFLGILLWFPKCDIKMTQSPSMVSLGERVTITKASQDINSYLSWFQK 62
 QY 61 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTTFFG 120
 DB 63 GKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTTFFG 122
 QY 121 GKLETKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVL 180
 DB 123 GKLETKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGVL 182
 QY 181 NSWTQDQSKDSTYSMSSTLTLLKDEYERHNSYTCEATHKTSPIVKSFNNEC 234
 DB 183 NSWTQDQSKDSTYSMSSTLTLLKDEYERHNSYTCEATHKTSPIVKSFNNEC 236

RESULT 13
 US-09-791-537-114644
 ; Sequence 114644, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
 ; TITLE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 114644

; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: synthetic construct
 US-09-791-537-114644

Query Match 79.0%; Score 974.5; DB 21; Length 235;
 Best Local Similarity 80.9%; Pred. No. 4.1e-77;
 Matches 190; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 1 MSVLTQVALLLLWLTGARCIDQMTQSPASLSASVGETVITCRASGNIONYLAWYQOQT 59
 DB 1 MKQSTIALALLPLLFPTVTRADIELTQSPALMAASVGETVITCGASENIYALNNYQK 60
 QY 60 QKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTTFFG 119
 DB 61 QKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSLOPEDFGSYCYQHFWSTPTTFFG 120
 QY 120 GGTLETKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGV 179
 DB 121 AGTKLETKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSRONGV 180
 QY 180 LNSWTQDQSKDSTYSMSSTLTLLKDEYERHNSYTCEATHKTSPIVKSFNNEC 234
 DB 181 LNSWTQDQSKDSTYSMSSTLTLLKDEYERHNSYTCEATHKTSPIVKSFNNEC 235

RESULT 14
 US-08-480-120-4
 ; Sequence 4, Application US/08480120
 ; GENERAL INFORMATION:
 ; APPLICANT: Joliffe, Linda K.
 ; APPLICANT: Pulito, Robert A.
 ; APPLICANT: Pulito, Virginia L.
 ; TITLE OF INVENTION: CDR-CRAFTED ANTI-TISSUE FACTOR
 ; TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,120
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 9598
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-480-120-4

Query Match 78.6%; Score 970; DB 8; Length 234;
 Best Local Similarity 78.2%; Pred. No. 1e-76;
 Matches 183; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSVLTQVALLLLWLTGARCIDQMTQSPASLSASVGETVITCRASGNIONYLAWYQOQT 60

1 MRAPQPFGLILLWFPICIRDKWTQSPSSWYASLGERVTITCKASQDIRKYLWYQOKP 60
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTOYSLKINSLOPEDFGSYCQHFWSPTPYTFGG 120
61 WKSPTLIYYATSLADGVPSRFGSGSGQDYSLTISLESDDTATYYCLOHGESPYPYTFGG 120
121 GTKLEIKRADAAPTIVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVL 180
121 GTKLEINRADAAPTIVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVL 180
181 NSWTDQDSKDYSTMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNNEC 234
181 NSWTDQDSKDYSTMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNNEC 234

RESULT 15
US-09-791-537-128696
Sequence 128696, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791.537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 128696
LENGTH: 234
TYPE: PRT
ORGANISM: Mus musculus
US-09-791-537-128696

Query Match 78.4%; Score 967; DB 21; Length 234;
Best Local Similarity 77.8%; Pred. No. 1.9e-76;
Matches 182; Conservative 18; Mismatches 34; Indels 0; Gaps 0;
1 MSLVTQVALLLLWLTGARCIDIOMTQSPASLSASVGETVTITCRASGNIONYLANWQOQTQ 60
1 MPTPAQPLGLILLWFPICIRDKWTQSPSSWYASLGERVTITCKASQDIRKYLWYQOKP 60
61 GKSPQLLVYSAKTLADGVPSRFGSGSGTOYSLKINSLOPEDFGSYCQHFWSPTPYTFGG 120
61 GKSPKTLIYRANLVDGVPSRFGSGSGQDYSLTISLESDDTATYYCLOHGESPYPYTFGG 120
121 GTKLEIKRADAAPTIVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVL 180
121 GTKLEINRADAAPTIVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVL 180
181 NSWTDQDSKDYSTMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNNEC 234
181 NSWTDQDSKDYSTMSSTLTLTDEYERHNSYTCETHKTSPIVKSFNNEC 234

Search completed: June 18, 2003, 16:56:49
Job time: 146.935 secs

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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:46:17 ; Search time 22.0197 Seconds
(without alignments)
1149.899 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVLALLLLWLTGARC.....EATHKTSPIVKSFRNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications:AA:*

- 1: /cgn2_5/ptodata/2/pubaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	925	75.0	238	9	US-09-903-327A-4
2	918	74.4	238	9	US-10-216-484-11
3	883.5	71.6	235	9	US-09-795-515-5
4	870	70.5	672	9	US-09-900-766-1
5	816	66.1	236	9	US-10-006-593-69
6	808	65.5	234	10	US-09-740-002-24
7	806	65.3	237	9	US-10-194-975-109
8	799	64.7	236	10	US-09-859-053-30
9	772.5	62.6	234	10	US-09-740-002-26
10	771	62.5	234	10	US-09-800-729-150
11	766	62.1	214	9	US-10-153-382-19
12	761	61.7	245	9	US-09-797-941A-6
13	756.5	61.3	235	10	US-09-800-729-152
14	754	61.1	237	9	US-10-020-786-8
15	754	61.1	237	9	US-10-227-694-4
16	751	60.9	237	9	US-10-227-694-1
17	751	60.9	237	10	US-09-056-160B-100
18	751	60.9	237	10	US-09-940-166A-6
19	751	60.9	491	12	US-10-011-125-2

ALIGNMENTS

RESULT 1

US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Eiquang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match

Best Local Similarity 75.0%; Score 925; DB 9; Length 238;
Matches 174; Conservative 27; Mismatches 33; Indels 4; Gaps 1;
Qy 1 MSVLTVLALLLLWLTGARDIQMTQSPASLSASVGETVTITCRASGNI-----ONLYAWY 56
Db 1 MEYDTILLWLLWVPGSTGDIVLTQSPASLSVSLGORATISCRASVSDYDGSYNNWY 60
Qy 57 QQTQGSQPLLVSATKLADVPFSRFGSGSGTQYSLKINSLOPEDFGSYCQHFSTPY 116
Db 61 QKPGQPKLLIYAASNLSESIPIARFSGSGGTDTFLNIHPVEEDATYTCQQTNEPDW 120
Qy 117 TFGGGTKLEIKRADAAPTVSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 176
Db 121 TFGGGTKLEIKRADAAPTVSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 180

20 744 60.3 214 10 US-09-940-166A-2 Sequence 2, Appli
21 744 60.3 214 10 US-09-811-384-11 Sequence 11, Appli
22 744 60.3 237 9 US-10-020-786-10 Sequence 10, Appli
23 744 60.3 240 10 US-09-799-514-8 Sequence 8, Appli
24 743 60.2 238 9 US-10-216-484-127 Sequence 127, App
25 742 60.1 238 9 US-10-216-484-131 Sequence 131, App
26 739 59.9 238 9 US-10-216-484-129 Sequence 129, App
27 736 59.6 214 9 US-10-253-366-1 Sequence 1, Appli
28 732 59.3 218 10 US-09-920-171-15 Sequence 15, Appli
29 732 59.3 218 10 US-09-920-171-17 Sequence 17, Appli
30 732 59.3 218 10 US-09-920-171-19 Sequence 19, Appli
31 732 59.3 218 10 US-09-920-171-24 Sequence 24, Appli
32 732 59.3 239 10 US-09-825-012-9 Sequence 9, Appli
33 730 59.2 218 9 US-09-1925-179-9 Sequence 9, Appli
34 730 59.2 218 10 US-09-802-077-9 Sequence 9, Appli
35 730 59.2 218 10 US-09-802-096-9 Sequence 9, Appli
36 730 59.2 218 10 US-09-920-171-13 Sequence 13, Appli
37 729.5 59.1 235 10 US-09-910-059-52 Sequence 52, Appli
38 727 58.9 212 12 US-10-011-125-5 Sequence 5, Appli
39 725.5 58.8 213 9 US-09-1996-288-211 Sequence 211, App
40 725.5 58.8 213 9 US-09-1996-265-211 Sequence 211, App
41 724 58.7 218 10 US-09-917-410-2 Sequence 2, Appli
42 724 58.7 220 10 US-09-917-410-5 Sequence 5, Appli
43 723.5 58.6 235 10 US-09-910-059-99 Sequence 99, Appli
44 723 58.6 214 9 US-09-1875-221A-128 Sequence 128, App
45 723 58.6 214 10 US-09-949-559-128 Sequence 128, App

177 NGVLSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 234
181 NGVLSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 238

RESULT 2
Sequence 11, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1ufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Takaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
LENGTH: 238
TYPE: PRT
ORGANISM: Mus musculus
US-10-216-484-11

Query Match 74.4%; Score 918; DB 9; Length 238;
Best Local Similarity 72.38; Pred. No. 1.3e-38;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

1 MSLVTQVLALLLWLTG--ARCDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWY 56
1 METDTILLWMLWIPGSGTGVILVTQSPASLAVSLGQRATISCKRASQSDVDGDSYNNY 60

57 QOTGKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPDEFGSYCQHFWSPTYP 116
61 QOKPGQPPKLLIYAASNLSEGPAPRFGSGSGTDTFTLNIHVEEEDAATYYCQOSNEDPR 120

117 TFGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVWCFLNNFYPKIDNVKWKIDGSRQ 176
121 TFGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVWCFLNNFYPKIDNVKWKIDGSRQ 180

177 NGVLSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 234
181 NGVLSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 238

RESULT 3
Sequence 5, Application US/09795515
Publication No. US2003003965A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yako
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-795-515-5

Query Match 71.6%; Score 883.5; DB 9; Length 235;
Best Local Similarity 72.08; Pred. No. 6.3e-37;
Matches 170; Conservative 21; Mismatches 42; Indels 3; Gaps 2;

1 MSLVTQVLALLLWLTG--ARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQ 58
1 MDFQVQIFSFLLISASVIRGQIVLTQSPALMSASPGCKVTMTCSASSV-SYNNWYQQ 59

59 TQGKSPQLLYVSAKTLADGVPSRFGSGSGTQYSLKINSLOPDEFGSYCQHFWSPTYP 118
60 KSGTSPKRWIYDTKSLASGVPAPRFGSGSGTQYSLTISGMEADAATYYCQOSNPTFF 119

119 GGGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVWCFLNNFYPKIDNVKWKIDGSRQ 178
120 GSGKLEIKRADAAPTVSIFFPSSSEOLTSGGASVWCFLNNFYPKIDNVKWKIDGSRQ 179

179 VLNSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 234
180 VLNSWTDQSDKSDSTYSMSSTLTLTLDKDEYERHNSYTCETHKSTSTPIVKSFNREC 235

RESULT 4
US-09-900-766-1
Sequence 1, Application US/09900766
Publication No. US2003003965A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 672
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(672)
OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 70.5%; Score 870; DB 9; Length 672;
Best Local Similarity 73.8%; Pred. No. 6.5e-36;
Matches 169; Conservative 20; Mismatches 36; Indels 4; Gaps 1;

QY 5 TQVLLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIONLYAWYQQTQKSP 64
Db 447 TSLISLYLT---SVMTQTPTSLVSGDRVTITCKASQSVNDVAVYQKPGQSP 502
QY 65 QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKL 124
Db 503 KLLYSYRVRAGVPDRFGSGYGTDFLTSSVQAEDAAVYFCQDYNSPPTFTGGTKL 562
QY 125 EIKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLSWT 184
Db 563 EIKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLSWT 622
QY 185 DQDSKDSYMSSTLTTLTKDEYERHNSYTCETHKTSTSPVKSFNNE 233
Db 623 DQDSKDSYMSSTLTTLTKDEYERHNSYTCETHKTSTSPVKSFNNE 671

RESULT 5

US-10-006-593-69
; Sequence 69, Application US/10006593
; Publication No. US20030045683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 236
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody light chain
US-10-006-593-69

Query Match 66.1%; Score 816; DB 9; Length 236;
Best Local Similarity 66.2%; Pred. No. 1.3e-33;
Matches 155; Conservative 28; Mismatches 51; Indels 0; Gaps 0;
QY 1 MSVLTQVLLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIONLYAWYQQTQ 60
Db 3 MRVPAQLLGLLLWLRGARDIQMTQSPSSLSASVGDRTVITTCASENIYCALNWKYQKP 62
QY 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120
Db 63 GKAPKLLIYAGNLHVRGVPDRFGSGSGTDFLTSSVQAEDAAVYFCQDYNSPPTFTGG 122
QY 121 GTKLEIKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVL 180
Db 123 GTKVEIKRVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 182
QY 181 NSWTDQDSKDSYMSSTLTTLTKDEYERHNSYTCETHKTSTSPVKSFNNEC 234
Db 183 ESVTEQDSKDSYMSSTLTSLRADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6

US-09-740-002-24
; Sequence 24, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-02/5759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-24

Query Match 65.5%; Score 808; DB 10; Length 234;
Best Local Similarity 64.5%; Pred. No. 3.1e-33;
Matches 151; Conservative 29; Mismatches 54; Indels 0; Gaps 0;
QY 1 MSVLTQVLLALLLWLTGARDIQMTQSPASLSASVGETVITTCRASGNIONLYAWYQQTQ 60
Db 1 METPAQLLGLLLWLRGARDIQMTQSPSSLSASVGDRTVITTCRAGQRIASLNNYQHP 60
QY 61 GKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGG 120
Db 61 GKAPKLLIYAGNLHVRGVPDRFGSGSGTDFLTSSVQAEDAAVYFCQDYNSPPTFTGG 120
QY 121 GTKLEIKRADAAPTYSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVL 180
Db 121 GTKVEIKRVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 180
QY 181 NSWTDQDSKDSYMSSTLTTLTKDEYERHNSYTCETHKTSTSPVKSFNNEC 234
Db 181 ESVTEQDSKDSYMSSTLTSLRADYKHKVYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 7

US-10-194-975-109
; Sequence 109, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized chimeric D1.3 antibody
US-10-194-975-109

Query Match 65.3%; Score 806; DB 9; Length 237;
Best Local Similarity 68.5%; Pred. No. 4e-33;
Matches 150; Conservative 24; Mismatches 45; Indels 0; Gaps 0;
QY 16 TGARCDIQMTQSPASLSASVGETVITTCRASGNIONLYAWYQQTQKSPQLLVYSAKTLA 75
Db 19 TNAYAAIRMTQSPSSLSASVGDRTVITTCRASGNINHYLAWYQKPAKAPKLIYITTTLA 78
QY 76 DGVP-SRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKLEIKRADAAPT 135
Db 79 DGVP-SRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPTFTGGTKLEIKRADAAPT 138

136 SIFPPSEQLTSGASVWVFLNFPKIDINVKWIDGSRQNGVLNSWTDQSDKSTYSM 195
139 FIFPPDEQLKSTASVYCLNLFYPREAKVQWVDNALQSGNSQESVTPEDQSDKSTYSL 198
196 SSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNNEC 234
199 SSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 8
S-09-859-053-30
Sequence 30, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsumari
APPLICANT: Hori, No. US20020102658A1uaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 64.7%; Score 799; DB 10; Length 236;
Best Local Similarity 64.5%; Pred. No. 8.7e-33;
Matches 151; Conservative 30; Mismatches 53; Indels 0; Gaps 0;

1 MSVLTQVLALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60
3 MRVPAQLLGLLLWLPFGSRCDIOMTQSPSSVSVSGVDRVTITTCRASGISRLAWYQOKP 62
61 GKSPOLLVYSAKTLADGVPSRFGSGGTQVSLKINSLOPEDFGSYCQHFWSPTFTFG 120
63 GKAPKLLIYVASSLQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSPFTFG 122
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVWVFLNFPKIDINVKWIDGSRQNGVL 180
123 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWVDNALQSGNSQ 182
181 NSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNNEC 234
183 ESVTEQSDKSTYLSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 9
S-09-740-002-26
Sequence 26, Application US/09740002
Patent No. US20020001798A1
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
US-09-740-002-26

Query Match 62.6%; Score 772.5; DB 10; Length 234;
Best Local Similarity 62.7%; Pred. No. 1.7e-31;
Matches 146; Conservative 37; Mismatches 49; Indels 1; Gaps 1;

1 MSVLTQVLALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60
3 MRVPAQLLGLLLWLPFGSRCDIOMTQSPSSVSVSGVDRVTITTCRASGISRLAWYQOKP 62
61 GKSPOLLVYSAKTLADGVPSRFGSGGTQVSLKINSLOPEDFGSYCQHFWSPTFTFG 120
63 GKAPKLLIYVASSLQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSPFTFG 122
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVWVFLNFPKIDINVKWIDGSRQNGVL 180
123 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWVDNALQSGNSQ 182
181 NSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNNEC 234
183 ESVTEQSDKSTYLSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 10
US-09-800-729-150
Sequence 150, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 150
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (120)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-150

Query Match 62.5%; Score 771; DB 10; Length 234;
Best Local Similarity 61.1%; Pred. No. 2e-31;
Matches 143; Conservative 36; Mismatches 55; Indels 0; Gaps 0;

1 MSVLTQVLALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRASGNIQNYLAWYQQTQ 60
1 MRVPAQLLGLLLWLPFGSRCDIOMTQSPSSVSVSGVDRVTITTCRASGISRLAWYQOKP 60
61 GKSPOLLVYSAKTLADGVPSRFGSGGTQVSLKINSLOPEDFGSYCQHFWSPTFTFG 120
63 GKAPKLLIYVASSLQSGVPSRFGSGGTDTFTLTISLQPEDFATYTCQANSPFTFG 122
121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVWVFLNFPKIDINVKWIDGSRQNGVL 180
123 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWVDNALQSGNSQ 182
181 NSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTCATHKTSPIVKSFNNEC 234
183 ESVTEQSDKSTYLSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 236

Db 181 ESVTEQDSKDYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 11

US-10-153-382-19

; Sequence 19, Application US/10153382

; Publication No. US20030086930A1

; GENERAL INFORMATION:

; APPLICANT: PFIZER PRODUCTS INC.

; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES

; FILE REFERENCE: PC23019A

; CURRENT APPLICATION NUMBER: US/10/153,382

; PRIOR FILING DATE: 2002-05-22

; PRIOR APPLICATION NUMBER: 60/293042

; PRIOR FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 19

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-153-382-19

Query Match 62.1%; Score 766; DB 9; Length 214;

Best Local Similarity 65.9%; Pred. No. 3.4e-31;

Matches 141; Conservative 32; Mismatches 41; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTGKSPQLLYSAKTLADGVPS 80

Db 1 DIQMTQSPSSLSASVGDRTVITTCRASGNITQNYLAWYQQTGKSPQLLYSAKTLADGVPS 60

QY 81 RFSGGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTFCGGTKLEIKRADAAPTYSIFPP 140

Db 61 RFSGGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTFCGGTKLEIKRADAAPTYSIFPP 120

QY 141 SSEQLTSGGASVVCFLNNFYPKDINVKKIDGSEKQNGVLSNWTQDSDKDYSLSTLT 200

Db 121 SDEQLKSTASVVCFLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180

QY 201 LTKDEYRHNSYTCETHKTSPTIVKSFNRNEC 234

Db 181 LSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 12

US-09-797-941A-6

; Sequence 6, Application US/09797941A

; Patent No. US20020164788A1

; GENERAL INFORMATION:

; APPLICANT: ELLIS, JONATHAN H.

; LEWIS, ALAN P.

; TITLE OF INVENTION: HUMANISED ANTIBODIES TO CD38

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/797,941A

; FILING DATE: 05-Mar-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/849,410

; FILING DATE: 30-MAY-1997

; APPLICATION NUMBER: PCT/GB95/02777

; FILING DATE: 28-NOV-1995

; APPLICATION NUMBER: GB 9424449.8

; FILING DATE: 02-DEC-1994

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 245 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-797-941A-6

Query Match 61.7%; Score 761; DB 9; Length 245;

Best Local Similarity 61.8%; Pred. No. 6.6e-31;

Matches 141; Conservative 32; Mismatches 55; Indels 0; Gaps 0;

QY 7 VLALLLMTGARCIDIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTGKSPQL 66

Db 18 IILFLVATATGVHSDIQMTQSPSSLSASVGDRTVITTCASEDIYRLTWYQKPGKAPKL 77

QY 67 LYSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTFCGGTKLEI 126

Db 78 LISGATSLGTGVPSRFSGGSGTDFTTTISLQPEDIATYCCQYWSNPYTFGGTKVEI 137

QY 127 KRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSEKQNGVLSNWTQ 186

Db 138 KRTVAAPSVFIFFPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQESVTEQ 197

QY 187 DSKDYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRNEC 234

Db 198 DSKDYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 245

RESULT 13

US-09-800-729-152

; Sequence 152, Application US/09800729

; Patent No. US20020068319A1

; GENERAL INFORMATION:

; APPLICANT: Ni et al.

; TITLE OF INVENTION: 32 Human secreted proteins

; FILE REFERENCE: P2044P1

; CURRENT APPLICATION NUMBER: US/09/800,729

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: PCT/US00/26013

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155,709

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 152

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-800-729-152

Query Match 61.3%; Score 756.5; DB 10; Length 235;

Best Local Similarity 62.0%; Pred. No. 1.1e-30;

Matches 145; Conservative 31; Mismatches 57; Indels 1; Gaps 1;

QY 1 MSVLTVLALLLMTGARCIDIQMTQSPASLSASVGETVITTCRASGNITQNYLAWYQQTQ 60

Db 3 MRVPAQLGLGLLWLGRARCQMGTQSPSSLSASVGDRTVITTCRTSQSIGKFLNNYQKPK 62

QY 61 GKSPLLTVYSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCOHFWSTPTTFCGG 120

Db 63 GQAPKLLISGASILQTVPSRFSGGSGSATYFTLTINDLHPDSATYCCQDYTPP-LFQQ 121

QY 121 GTKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSEKQNGVL 180

Db 122 GTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCFLNNFYPREAKVQKVDNALQSGNSQ 181

QY 181 NSWTQDSDKDYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRNEC 234

db 182 ESVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 14

JS-10-020-786-8

Sequence 8, Application US/10020786

Publication No. US20030073164A1

GENERAL INFORMATION:

APPLICANT: Simmons, Laura C.

APPLICANT: Klimowski, Laura

APPLICANT: Reilly, Dorothea

APPLICANT: Yansura, Daniel G.

TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF

FILE REFERENCE: P1793R1

CURRENT APPLICATION NUMBER: US/10/020,786

CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 60/256,164

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 8

LENGTH: 237

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: anti-Tf light chain

JS-10-020-786-8

Query Match 61.1%; Score 754; DB 9; Length 237;

Best Local Similarity 64.4%; Pred. No. 1.4e-30;

Matches 141; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

16 TGARCDIQMTPASLSASVGETVTITCRASGNIONYLAWYQOTGKSPOLLVYSAKTLA 75

19 TNAYADIQMTSPSSLSASVGDRTVITCRASRDIKSYLNNWYQQRPGKAPKVLIIYATSLA 78

76 DGVPSRFSGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTPTFGGGTKLEIKRADAAPTV 135

79 EGVPSRFSGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTPTFGGGTKLEIKRADAAPTV 138

136 SIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSWTDQDSKDYSTM 195

139 FIFPPSDQLKSGTASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSWTDQDSKDYSTM 198

196 SSTLTLTQDEYERHNSYTCETHKTSPTIVKSFNRNEC 234

199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

196 SSTLTLTQDEYERHNSYTCETHKTSPTIVKSFNRNEC 234

199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

196 SSTLTLTQDEYERHNSYTCETHKTSPTIVKSFNRNEC 234

199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

196 SSTLTLTQDEYERHNSYTCETHKTSPTIVKSFNRNEC 234

199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 15

US-10-227-694-4

Sequence 4, Application US/10227694

Publication No. US2003007739A1

GENERAL INFORMATION:

APPLICANT: Simmons, Laura

APPLICANT: Andersen, Dana

TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY

FILE REFERENCE: P1867R1

CURRENT APPLICATION NUMBER: US/10/227,694

CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: US 60/315,209

PRIOR FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 4

LENGTH: 237

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-227-694-4

Query Match 61.1%; Score 754; DB 9; Length 237;

Best Local Similarity 64.4%; Pred. No. 1.4e-30;

Matches 141; Conservative 32; Mismatches 46; Indels 0; Gaps 0;

QY 16 TGARCDIQMTPASLSASVGETVTITCRASGNIONYLAWYQOTGKSPOLLVYSAKTLA 75
 Db 19 TNAYADIQMTSPSSLSASVGDRTVITCRASRDIKSYLNNWYQQRPGKAPKVLIIYATSLA 78
 QY 76 DGVPSRFSGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTPTFGGGTKLEIKRADAAPTV 135
 Db 79 EGVPSRFSGSGGTQYSLKINSLOPEDFGSYQCQHFWSPTPTFGGGTKLEIKRADAAPTV 138
 QY 136 SIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSWTDQDSKDYSTM 195
 Db 139 FIFPPSDQLKSGTASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSWTDQDSKDYSTM 198
 QY 196 SSTLTLTQDEYERHNSYTCETHKTSPTIVKSFNRNEC 234
 Db 199 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

Search completed: June 18, 2003, 16:58:02
 Job time : 23.0197 secs

OM protein - protein search, using sw model

Run on:

June 18, 2003, 16:42:37 ; Search time 11.5028 Seconds
(without alignments)
598.546 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLTVQVLLALLLWLTGARC.....EATHTSTSPVKSFRNEC 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/6C.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	97.2	234	5	PCT-US94-07659-4
2	1131	91.7	236	2	US-08-792-824-3
3	1131	91.7	236	2	US-08-792-824-3
4	1131	91.7	236	2	US-08-792-824-9
5	1080	87.5	233	2	US-08-792-824-12
6	955	77.4	234	2	US-08-792-824-6
7	930.5	75.4	239	1	US-07-690-192-2
8	924	74.9	235	2	US-08-353-400-37
9	907.5	73.5	235	4	US-08-737-129A-8
10	907.5	73.5	235	4	US-09-423-439-58
11	907	73.5	211	4	US-09-011-769A-23
12	901	73.0	218	5	PCT-US94-14106-57
13	888.5	72.0	219	1	US-08-353-400-34
14	883.5	71.6	235	2	US-08-303-569B-5
15	883.5	71.6	235	2	US-08-116-247-5
16	881.5	71.4	238	3	US-09-192-545-4
17	868	70.3	213	2	US-08-737-129A-4
18	855.5	69.3	215	6	5455030-3
19	845	68.5	215	4	US-09-170-769A-4
20	818	66.3	218	5	PCT-US94-14106-61
21	792	64.2	236	1	US-08-157-101A-5
22	790	64.0	206	6	5189147-9
23	771	62.5	214	3	US-08-397-411-5
24	759	61.5	233	2	US-07-934-373C-25
25	759	61.5	233	3	US-08-437-642B-25
26	759	61.5	233	4	US-08-146-206C-25
27	759	61.5	233	5	PCT-US93-07832-25

28	756.5	61.3	232	1	US-08-704-744-80
29	751	60.9	237	3	US-09-097-309-6
30	751	60.9	237	4	US-09-097-171A-10
31	751	60.9	237	4	US-09-422-712B-2
32	751	60.9	237	4	US-09-607-756-2
33	751	60.9	237	4	US-09-460-587-6
34	748	60.6	235	3	US-08-812-586-16
35	745	60.4	214	2	US-07-934-373C-39
36	745	60.4	214	3	US-08-437-642B-39
37	745	60.4	214	5	PCT-US93-07832-39
38	744	60.3	214	2	US-07-934-373C-40
39	744	60.3	214	2	US-08-788-800-11
40	744	60.3	214	3	US-08-437-642B-40
41	744	60.3	214	4	US-09-097-309-2
42	744	60.3	214	4	US-09-097-171A-2
43	744	60.3	214	4	US-09-460-587-2
44	744	60.3	214	5	PCT-US93-07832-40
45	743	60.2	237	2	US-08-463-587A-25

ALIGNMENTS

RESULT 1
PCT-US94-07659-4
; Sequence 4, Application PC/TUS9407659

; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07659
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,534
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50171-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07659-4

Query Match

97.2% ; Score 1200; DB 5; Length 234;

us-09-770-916-4.rai

ue Jul 1 18:41:06 2003

Best Local Similarity 97.0%; Pred. No. 5.3e-90; Indels 0; Gaps 0;
 Matches 227; Conservative
 1 MSVLTQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 60
 1 MSVLTQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 60
 61 GKSQQLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120
 61 GKSQQLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 120
 121 GTKLEIKRADAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVL 180
 121 GTKLEIKRADAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGVL 180
 181 NSWTDQSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234
 181 NSWTDQSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234
 181 NSWTDQSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234

RESULT 2
 US-08-792-824-3
 : Sequence 3, Application US/08792824
 : Patent No. 5932449
 : GENERAL INFORMATION:
 : APPLICANT: EMANUEL, PETER A.
 : APPLICANT: BURANS, JAMES P.
 : APPLICANT: VALDES, JAMES J.
 : APPLICANT: MOHVEE, ELDEFRAWI E.
 : TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: U.S. Army Chemical and Biological Defense
 : ADDRESS: Command
 : STREET: Office of the Chief Counsel, Bldg E4435
 : CITY: Aberdeen Proving Ground
 : STATE: MD
 : COUNTRY: U.S.
 : ZIP: 21010-5423
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/792,824
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Biffoni, U. J.
 : REGISTRATION NUMBER: 39,908
 : REFERENCE/DOCKET NUMBER: DAM 431-96
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 410-671-1158
 : TELEFAX: 410-671-2534
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 236 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-792-824-3

Query Match 91.7%; Score 1131; DB 2; Length 236;
 Best Local Similarity 93.9%; pred. No. 2.1e-84; Indels 0; Gaps 0;
 Matches 216; Conservative
 5 TQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 64
 7 TAAAGLLLLAAQPAMADIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 66
 QY
 Db

Db 67 QLLVYNKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGGG 126
 QY 125 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGV 184
 Db 127 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGV 186
 QY 185 DQSDKSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234
 Db 187 DQSDKSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 236

RESULT 3
 US-08-792-824-9
 : Sequence 9, Application US/08792824
 : Patent No. 5932449
 : GENERAL INFORMATION:
 : APPLICANT: EMANUEL, PETER A.
 : APPLICANT: BURANS, JAMES P.
 : APPLICANT: VALDES, JAMES J.
 : APPLICANT: MOHVEE, ELDEFRAWI E.
 : TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: U.S. Army Chemical and Biological Defense
 : ADDRESS: Command
 : STREET: Office of the Chief Counsel, Bldg E4435
 : CITY: Aberdeen Proving Ground
 : STATE: MD
 : COUNTRY: U.S.
 : ZIP: 21010-5423
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/792,824
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Biffoni, U. J.
 : REGISTRATION NUMBER: 39,908
 : REFERENCE/DOCKET NUMBER: DAM 431-96
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 410-671-1158
 : TELEFAX: 410-671-2534
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 236 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-792-824-9

Query Match 91.7%; Score 1131; DB 2; Length 236;
 Best Local Similarity 93.9%; pred. No. 2.1e-84; Indels 0; Gaps 0;
 Matches 216; Conservative
 5 TQVALLLWLTGARGDIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 64
 7 TAAAGLLLLAAQPAMADIQMTQSPASLSASVGETVITCRASGNIONYLAWYQQTQ 66
 QY
 Db 65 QLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 124
 QY 67 QLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTFTGG 126
 Db 125 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGV 184
 QY 127 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRONGV 186
 Db 185 DQSDKSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 234
 QY 187 DQSDKSDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNREC 236
 Db

RESULT 4

```

US-08-792-824-12
; Sequence 12, Application US/08792824
; Patent No. 5952449
;
; GENERAL INFORMATION:
;
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN

```

Query Match	91.7%	Score 1131;	DB 2;	Length 236;
Best Local Similarity	93.9%	Pred. No. 2.1e-84;		
Matches 216; Conservative	2;	Mismatches 12;	Indels 0;	Gaps 0;

RESULT 5

US-08-792-824-6
; Sequence 6, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.

;	APPLICANT:	VALDES, JAMES J.	
;	APPLICANT:	MOHYEE, ELDEFRAWI E.	
;	TITLE OF INVENTION:	DETECTION OF BOTULINUM TOXIN	
;	NUMBER OF SEQUENCES:	13	
;	CORRESPONDENCE ADDRESS:		
;	ADDRESSEE:	U.S. Army Chemical and Biological Defense	
;	ADDRESSEE:	Command	
;	STREET:	Office of the Chief Counsel, Bldg E4435	
;	CITY:	Aberdeen Proving Ground	
;	STATE:	MD	
;	COUNTRY:	U.S.	
;	ZIP:	21010-5423	
;	COMPUTER READABLE FORM:		
;	MEDIUM TYPE:	Floppy disk	
;	COMPUTER:	IBM PC compatible	
;	OPERATING SYSTEM:	PC-DOS/MS-DOS	
;	SOFTWARE:	Patentin Release #1.0, Version #1.30	
;	CURRENT APPLICATION DATA:		
;	APPLICATION NUMBER:	US/08/792,824	
;	FILING DATE:		
;	CLASSIFICATION:	435	
;	ATTORNEY/AGENT INFORMATION:		
;	NAME:	Biffoni, U. J.	
;	REGISTRATION NUMBER:	39,908	
;	REFERENCE/DOCKET NUMBER:	DAM 431-96	
;	TELECOMMUNICATION INFORMATION:		
;	TELEPHONE:	410-671-1158	
;	TELEFAX:	410-671-2534	
;	INFORMATION FOR SEQ ID NO:	6:	
;	SEQUENCE CHARACTERISTICS:		
;	LENGTH:	233 amino acids	
;	TYPE:	amino acid	
;	TOPOLOGY:	linear	
;	MOLECULE TYPE:	protein	
;	US-08-792-824-6		
;	Query Match	87.5%;	Score 1080; DB 2; Length
;	Best Local Similarity	92.0%;	Pred No. 2.8e-80;
;	Matches 206;	Conservative 5;	Mismatches 13; Indels
QY	5	TQVLAALLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNIGN	
Db	7	TAAAGLLLLAQAQMADITQSPASLSASVGETVTITCRASGNIGN	
QY	65	QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSIQPEDFGSGYCYQH	
Db	67	QLLVYNAKTLADGVPSRFGSGSGTQYSLKINSIQPEDFGSGYCYQH	
QY	125	EIKRADAAPTVSIFPPPSSEQLTSGGASVCFLLNFPKIDINVKKWID	
Db	127	EIKRADAAPTVSIFPPPSSEQLTSGGASVCFLLNFPKIDINVKKWID	
QY	185	DQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSIPVKS 22	
Db	187	DQSKDSTYSMSSTLTITKDEYERHNSYTCETHKTSIPVKS 23	
;	RESULT 6		
;	US-07-690-192-2		
;	Sequence 2, Application	US/07690192	
;	Patent No.	5919650	
;	GENERAL INFORMATION:		
;	APPLICANT:	Montano, Ximena	
;	APPLICANT:	Barbacid, Mariano	
;	TITLE OF INVENTION:	METHOD FOR INACTIVATION OF PROTEIN	
;	TITLE OF INVENTION:	METHOD FOR INACTIVATION OF PROTEIN	
;	NUMBER OF SEQUENCES:	4	
;	CORRESPONDENCE ADDRESS:		
;	ADDRESSEE:	Bristol-Myers Squibb Company	
;	STREET:	P.O. Box 4000	
;	CITY:	Princeton	
;	STATE:	New Jersey	
;	COUNTRY:	U.S.A.	

us-09-770-916-4.ra1

Tue Jul 1 18:41:06 2003

ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/690,192
APPLICATION NUMBER: 19910422
FILING DATE: 19910422
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Boyden, James M
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: DC13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-07-690-192-2

Query Match 77.4%; Score 955; DB 2; Length 234;
Best Local Similarity 76.9%; Pred. No. 3.7e-70;
Matches 180; Conservative 25; Mismatches 29; Indels 0; Gaps 0;
1 MSVLTQVIALLLWLTGARGDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLA 60
1 MAIPTQLGLLLWLTDAICDIQMTQSPHLSLSIGETVSTECASEGISNYLAWYQKP 60
61 GKSPQLIYVSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCQHFWSPTYFGG 120
61 GKSPQLIYVSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCQHFWSPTYFGG 120
121 GTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVWCFNNFYPKDINVKWIDGSRONGVL 180
121 GTKLEIKRADAAPTVSIFFPPSSEQLTSGGASVWCFNNFYPKDINVKWIDGSRONGVL 180
181 NSWTDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234
181 DSVTDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234

RESULT 7
US-08-353-400-37
Sequence 37, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-37
Query Match 75.4%; Score 930.5; DB 1; Length 239;
Best Local Similarity 75.0%; Pred. No. 3.6e-66;
Matches 180; Conservative 22; Mismatches 31; Indels 7; Gaps 2;
QY 1 MSVLTQVIALLLWLTGARGDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLA 54
DB 1 MDSQAQVLIALLWVSGTCGDIVMSQSPSSLAWSAGEKVTMSCKSSQSLNSTRKKNYLA 60
QY 55 WYQOTQCKSPQLIYVSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCQHFWS 114
DB 61 WYQORPGOSPKLLIYVSAKTLADGVPSRFSGGSGTQYSLKINSLOPEDFGSYCQHFWS 119
QY 115 PYTFGGGTGKLEIKRADAAPTVSIFFPPSSEQLTSGGASVWCFNNFYPKDINVKWIDGSE 174
DB 120 LRTEGGGTGKLEIKRADAAPTVSIFFPPSSEQLTSGGASVWCFNNFYPKDINVKWIDGSE 179
QY 175 RQGVLSNWTDDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234
DB 180 RQGVLSNWTDDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 239

RESULT 8
US-08-737-129A-8
Sequence 8, Application US/08737129A
Patent No. 5885816
GENERAL INFORMATION:
APPLICANT: Ikuo FUJII et al.
TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,129A
FILING DATE: No. 5885816ember 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-129A-8
Query Match 74.9%; Score 924; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 1.1e-67;

Matches	174;	Conservative	15;	Mismatches	25;	Indels	0;	Gaps	0;
Qy	21	DIQMTSPASLSASVGETVTITCRASGNITONYLAWVQOTQCKSPQLLVYSAKTTLADGVPS	80						
Db	1	ELVYQTPTSSMYASLGERVTITCKASQDINILYUSWFQKPGKSPKALIVYRTNGLVDGVPS	60						
Qy	81	RFGSGSGTGYSLKINSLOPEFGSYCYOHFWSTPYTFGGGTGKLEIKRADAAPTYSIFPP	140						
Db	61	RFGSGSGGDYSLTISLSEYEDMGIVCYQYDEFPTYFGGGTKLEIKRADAAPTYSIFPP	120						
Qy	141	SSEQLTSGGASVVCFLNNFPYKDIVNKKWIDGSEKQNGVLNSWTQDQSKDSTYSMSSTLT	200						
Db	121	SSEQLTSGGASVVCFLNNFPYKDIVNKKWIDGSEKQNGVLNSWTQDQSKDSTYSMSSTLT	180						
Qy	201	LTKDYEHRHNSYTCETHTKTSTSPIVKSFNRNEC	234						
Db	181	LTKDYEHRHNSYTCETHTKTSTSPIVKSFNRNEC	214						

RESULT 9
US-09-423-439-58
; Sequence 58, Application US/09423439
; Patent No. 639070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

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MIF: 20003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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SEQUENCE DESCRIPTION: SEQ ID NO: 58:
S-09-423-439-58

[illegible]

QY 179 VLNSWTDQDQSKDSTYMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
 Db 180 VLNSWTDQDQSKDSTYMSSTLTLLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 10
 US-09-011-769A-23
 ; Sequence 23, Application US/09011769A
 ; Patent No. 6436691
 ; GENERAL INFORMATION:
 ; APPLICANT: SLATER, Anthony M.
 ; BLAKEY, David C.
 ; DAVIES, David H.
 ; HENNAM, John F.
 ; HENNEQUIN, Laurent F.A.
 ; MARSHAM, Peter R.
 ; DOWELL, Robert I.
 ; TITLE OF INVENTION: Chemical Compounds
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, LLP
 ; STREET: 1100 New York Ave., N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
S-09-011-769A-23

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Query Match          73.5%; Score    907.5; DB 4; Length 235;  
Best Local Similarity 74.6%; Pred. No. 2.6e-66;  
Matches      Conservative   20; Mismatches   37; Indels       3; Gaps        2;
```

1 MSVLTQVLALLLL--WLTGARCDQTMTQSASLTSASGCVETVTITCRASGNIONYLAWYQQ 58
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
1 MDFQVOIFSFLLISASVIMSRGTVALSQSPAILLSAPCEKVTTCRASSY-TYIHWYQQ 59

59 TQGSKPOLLVYSAKTLADGVPSRFSSGSCTGYSLKINSIQPEDFGSVYCQHFWSTPYTF 118
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
60 KPGSSPKSWIATSNLASGVPA RFSSGSCTSYSLTISRVEADAATYYCQHWSKPPTF 119

119 GGGFKLLEIKRADAPTYSIIPPPSSELTSGGASVWCFLNNFYPKDINVWKIDGSERQNQ 178
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
120 GGGFKLLEIKRADAPTYSIIPPPSSELTSGGASVWCFLNNFYPKDINVWKIDGSERQNQ 179

179 VLNSWTDDQSDKDYTSMSSLTILTKLEYEHNYSYTCEATHKTSTPIVSFNNEC 234
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
180 VLNSWTDDQSDKDYTSMSSLTILTKLEYEHNYSYTCEATHKTSTPIVSFNNEC 235

Matches	Conservative	Mismatches	Indels	Gaps	
169;					1;
21	DIQMTQSPASLSASVGETVTTCR---	ASGNIQNYLAWYQQTQCKSPQLLVYSAKTLAD	76		
1	DIQMTQSPASLSASVGETVTTCR---	SSSHYMHVYQKQPGQPKLLIKYASNL	60		
77	GVPSRFSGSGLTQVSLKINSIQP	EDFGSYVYCOHFWSTPTFGGKLEIKRDAAPT	136		
61	GVPA	RFSGSGLTQVSLKINSIQP	EDFGSYVYCOHFWSTPTFGGKLEIKRDAAPT	120	
137	IFPPS	EQLTSGGASVVCFLNNFYFKDINVKWKIDGSE	RQNGVLNSWTDQDSKOSTYSMS	196	
121	IFPPS	EQLTSGGASVVCFLNNFYFKDINVKWKIDGSE	RQNGVLNSWTDQDSKOSTYSRS	180	
197	STLT	LKDEYERINSYTC	EAHTKSTSPVKSFNR	NEC 234	
181	STLT	LKDEYERINSYTC	EAHTKSTSPVKSFNR	NEC 218	

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Query Match	72.0%	Score	888.5	DB 1	Length	219;	
Best Local Similarity	77.3%	Pred.	No. 8.2e-65;				
Matches	170;	Conservative	20;	Mismatches	23;	Gaps	2;
	y	21	DIQMTQSPASLSASVGETVTITCRAGNI-----QNWLAWYQQTGKSPOLLIVYSAKTL	74			
	b	1	DIVMSGPSSLAVSAGEKVTWMSCKSQSLNSTRKNLYLAWYQRPQGSPKLLIYNASTR	60			
	y	75	ADGVPSRFSGSGGTQYSLKLINSLOPEDFGSYCQHFHWSTPTPTFGGTTKLEIKRADAAPT	134			
	b	61	TSGVPDRFTTGGSGGDFLTIIISVAEDLAITYCKQSY-TLRTEFGGTTKLEIKRADAAPT	119			
	y	135	VSIFFPSSSQLTSGGASVVCFLNNFPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYS	194			
	b	120	VSIFFPSSSQLTSGGASVVCFLNNFPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYS	179			
	y	195	MSSTLTILTKDEYRHHSNYTCEATHKTSTSPIVKSFNRRNEC	234			
	b	180	MSSTLTILTKDEYERHHSNYTCEATHKTSTSPIVKSFNRRNEC	219			

RESULT 14

[illegible]

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RESULT 12
PCT-US94-14106-57
Sequence 57, Application PC/TUS9414106
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Process for Generating Specific Antibodies
NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14106-57

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Query Match	73.0%;	score 901;	DB 5;	Length 218;
Best Local Similarity	77.5%;	Pred. No. 7.9e-66;		


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US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-303-569B-5

Query Match          71.6%; Score 883.5; DB 2; Length 235;
Best Local Similarity 72.0%; Pred. No. 2.3e-64;
Matches 170; Conservative 21; Mismatches 42; Indels 3; Gaps 3

QY      1 MSVLTVQLALLLLWLTG--ARCDIQMTQPASLSASVGETVTITCRASGNIQNYLA
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY      1 MDFQVQIFSLIASVIISRGQIVLITQSPAINMASPGKEKVTMTCSASSSV-SYMN
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY     59 TQGKSPLLVSAKTLADGVPSRFSGSGCTGYSLKINSLOPEDFGSYVCQHFWSTI
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY     60 KSGTSPRKWIYDTSKLASGVPAHFRGGSGGTYSVLTISGWAEADATYYCOQWSNN
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    119 GGGTKLEIKRADAAPTVISIPPPSEQLTSGGSASVVCFLNMFYPKDINVKWKIDGSE
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    120 GSGTKLEINRADTAPTVISIPPPSEQLTSGGSASVVCFLNMFYPKDINVKWKIDGSE
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    179 VLNSWTQDQSDKDSYSSMSTLTITKDEYDRHNSYTCEATHKTSTSPIVKSFNRNEC
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    180 VLNSWTQDQSDKDSYSSMSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
DB       |   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 15
US-08-116-247-5
; Sequence 5, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116.247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-116-247-5

	Query Match	71.6%	Score	883.5	DB 2	Length	235
	Best Local Similarity	72.0%	Pred.	No. 2.3e-64			
	Matches	170	Conservative	21	Mismatches	42	Indels
							Gaps
QY	1	MSVLTQVLALLLWLGT--	ARCQIDMTQSPASISASVGETVTITTCRASGNIQNYLANVQ	58			
DB	1	MDPQVIFSELLLSASV	IIRGQIVLTQSPAIMSASPGKVTWTCSSASSV-SYMNWYQ	59			
QY	59	TQKSGPOLLVYSAKT	LIADGVPSRFSGSGTQSYLKSINSLQPEDFGYSVYQCHFWSTPTTF	118			
DB	60	KSGTSPKRWTYDTS	KLASGVPAHFRGSGSGTSYSLTISGMEADAATYYCQOWSSNPFTF	119			
QY	119	GGCTKLEIKRADAAPTVS	IFPPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSEKQNG	178			
DB	120	GSGETKLEINRADTAPT	VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSEKQNG	179			
QY	179	VLSNWTDDQSDKDSY	MSSTLTITKDEYERHNSYTCETHKTSTPTVKSFNRNEC	234			
DB	180	VLSNWTDDQSDKDSY	MSSTLTITKDEYERHNSYTCETHKTSTPTVKSFNRNEC	235			

Search completed: June 18, 2003, 16:49:19
Job time : 12.5028 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 16:41:53 ; Search time 32.2079 Seconds
(without alignments)
968.107 Million cell updates/sec

Title: US-09-770-916-4

Perfect score: 1234

Sequence: 1 MSVLQVLALLLLWLTGARC.....EATHKTSTSPVVKSPNRNEC 234

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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23: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1200	97.2	234	16 AAW11918	Murine MAB SK48-E2
2	1131	91.7	236	20 AAY30116	Murine anti-botuli
3	1131	91.7	236	20 AAY30120	Murine anti-botuli
4	1131	91.7	236	20 AAY30122	Murine anti-botuli
5	1080	87.5	233	20 AAY30118	Murine anti-botuli
6	955	77.4	234	20 AAY14557	Anti-p21(ras) mono
7	947	76.7	214	18 AAW27089	Mouse monoclonal a
8	930.5	75.4	239	16 AAW76087	MAB 55.1 light cha
9	925	75.0	238	23 AAE18371	Human penton base
10	924	74.9	216	17 AAW15935	Antibody 3G2 light

11	918	74.4	238	19 AAW83042	Anti-Fas MAB HFE7A
12	918	74.4	238	21 AAB14748	Mouse anti-Fas ant
13	918	74.4	238	21 AAW90898	Murine anti-Fas an
14	918	74.4	238	23 ABB74867	Humanised anti-Fas
15	918	74.4	238	23 ABB74913	Humanised anti-Fas
16	909.5	73.7	235	15 AAR47449	T84.12 light chain
17	909.5	73.7	235	15 AAR47451	T84.12 L4-12-1 lig
18	909	73.7	220	15 AAR53802	FAB light chain fo
19	907.5	73.5	235	17 AAW06178	Murine A5B57 Light
20	907.5	73.5	235	20 AAW82746	Plasmid pPE14/A5B7
21	904.5	73.3	215	15 AAR53803	FAB light chain fo
22	902	73.1	223	5 AAP40031	Kappa anti-carcino
23	901.5	73.1	215	14 AAR43674	Mouse anti-bovine
24	901	73.0	218	16 AAR75457	Mouse antibody FB3
25	901	73.0	218	16 AAR75459	Mouse antibody F4-
26	897	72.7	222	18 AAW01751	MH1 monoclonal ant
27	896.5	72.6	215	17 AAR95644	Anti-BGH monoclonal
28	895.5	72.6	215	17 AAR97377	Murine anti-BGH MA
29	892	72.3	214	23 ABB76125	Recombinant 4G10 a
30	888.5	72.0	219	16 AAR76086	MAB 55.1 light cha
31	888	72.0	214	21 AAW78253	Mouse agglutinin
32	885.5	71.8	239	16 AAR68757	Anti-tobacco mosai
33	884.5	71.7	213	10 AAP93035	Chimeric antibody
34	884.5	71.7	238	18 AAW31752	L chain subunit of
35	884.5	71.7	238	19 AAW71889	Anti-human Fas mon
36	884.5	71.7	238	21 AAB12909	Anti-human Fas ant
37	883.5	71.6	235	12 AAR13060	Monoclonal antibod
38	881.5	71.4	238	20 AAY17416	Mouse immunoglobul
39	881	71.4	236	13 AAR22565	Villys-HuCKappa reg
40	878.5	71.2	573	22 AAG64459	Mouse 6D9 catalyti
41	875.5	70.9	213	22 AAM50205	Type II collagen f
42	874.5	70.9	219	21 AAY95258	WOW-1 Fab light ch
43	874.5	70.9	234	23 AAO72802	TRA-8 light chain
44	873	70.7	209	16 AAR64204	Monoclonal antibod
45	870.5	70.5	219	14 AAR44495	Sequence of the im

ALIGNMENTS

RESULT 1

AAW11918
ID, AAW11918 standard; Protein; 234 AA.

XX AAW11918;

XX '24-JUN-1997 (first entry)

DE Murine MAB SK48-E26 light chain.

Interleukin-1 beta; IL-1 beta; recombinant antibody;
humanised antibody; chimeric antibody; antibody engineering;
monoclonal antibody; MAB; SK48-E26; inflammation; therapy.

OS Homo sapiens.

XX Key

FT Peptide

FT Location/Qualifiers

FT 1..20

FT /label= Sig_peptide

FT 21..43

FT /label= FR1

FT /note= "framework region 1"

FT 44..54

FT /label= CDRI

FT /note= "complementarity determining region 1

FT (Claim 10, page 48)"

FT 55..69

FT /label= FR2

FT /note= "framework region 2"

FT 70..76

FT /label= CDR2

FT /note= "complementarity determining region 2

FT (Claim 10, page 48)"

Region	77..108	/label= FR3	/note= "framework region 3"
Region	109..117	/label= CDR3	/note= "complementarity determining region 3 (Claim 10, page 48)"
Region	118..127	/label= FR4	/note= "framework region 4"
Region	128..234	/label= Constant region	

RESULT 2
AAY30116
ID AAY30116 standard; Protein; 236 AA.
XX
AC AAY30116;

XX	20-OCT-1999	(first entry)
DT		
XX		
XX		
DE		
XX		
KW	Murine anti-botulinum toxin antibody fragment (BotFab 5) light chain.	
KW	Recombinant antibody fragment; rFab; botulinum; neurotoxin;	
KW	Clostridium botulinum; detection.	
XX		
OS	Mus musculus.	
XX		
PN	US5932449-A.	
XX		
PD	03-AUG-1999.	
XX		
PF	30-JAN-1997; 97US-0792824.	
XX		
XX	01-FEB-1996; 96US-0011013.	
PR	30-JAN-1997; 97US-0792824.	
XX		
XX	(USSA) US SEC OF ARMY.	
PA		
XX		
XX	Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;	
PI		
PI	WPI; 1999-492692/41.	
XX		
DR	N-PSDB; AAX86664.	
DR		
XX	Detection of botulinum toxin	
XX		
PT		
XX		
PS	Claim 1; Columns 17-20; 24pp; English.	
PS		
XX		
XX	This sequence represents the light chain of BotFab 5,	
CC	a murine recombinant antibody fragment (rFab) specific to	
CC	botulinum toxin types A and B. A cDNA library was made from mouse mRNA	
CC	isolated from mice immunised with human pentavalent toxoid. The cloned	
CC	mouse heavy and light chains were expressed in phage display libraries	
CC	and screened for their ability to bind to botulinum toxin types A or B.	
CC	The clones were then isolated and sequenced. Botulinum neurotoxin is	
CC	produced as several antigenically distinct serotypes (A-G) and is	
CC	non-covalently associated with non-neurotoxic proteins. The rFab of	
CC	this invention binds to the non-neurotoxic proteins that are found in	
CC	neurotoxin complexes A and B. Such antibody fragments are able to	
CC	act as immunosensors for detecting botulinum toxins in food and	
CC	are also useful in health care and in military applications. They	
CC	are less expensive to produce than monoclonal antibodies as they can be	
CC	isolated from large scale bacterial cultures. Also, the affinity of an	
CC	rFab may be altered by mutagenesis of its gene and subsequent screening	
CC	of the expressed rFabs.	

RESULT 3
AAY30120

AY30120 standard; Protein; 236 AA.
AY30120;
20-OCT-1999 (first entry)
Murine anti-botulinum toxin antibody fragment (BotFab 20) light chain.
Recombinant antibody fragment; rFab; botulinum; neurotoxin;
Clostridium botulinum; detection.
Mus musculus.
US5932449-A.
03-AUG-1999.
30-JAN-1997; 97US-0792824.
01-FEB-1996; 96US-0011013.
30-JAN-1997; 97US-0792824.
(USSA) US SEC OF ARMY.
Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;
WPI; 1999-492692/41.
N-PSDB; AAX86666.
Detection of botulinum toxin
Claim 15; Columns 31-34; 24pp; English.
This sequence represents the light chain of BotFab 20,
a murine recombinant antibody fragment (rFab) specific to
botulinum toxin types A and B. A cDNA library was made from mouse mRNA
isolated from mice immunised with human pentavalent toxoid. The cloned
mouse heavy and light chains were expressed in phage display libraries
and screened for their ability to bind to botulinum toxin types A or B.
The clones were then isolated and sequenced. Botulinum neurotoxin is
produced as several antigenically distinct serotypes (A-G) and is
non-covalently associated with non-neurotoxic proteins. The rFab of
this invention binds to the non-neurotoxic proteins. The rFab of
neurotoxin complexes A and B. Such antibody fragments are able to
act as immunosensors for detecting botulinum toxins in food and
are also useful in health care and in military applications. They
are less expensive to produce than monoclonal antibodies as they can be
isolated from large scale bacterial cultures. Also, the affinity of an
rFab may be altered by mutagenesis of its gene and subsequent screening
of the expressed rFabs.

Query Match 91.7%; Score 1131; DB 20; Length 236;
Best Local Similarity 93.9%; Pred. No. 2.2e-64;
Matches 216; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
QY 5 TQVLALLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQKSP 64
DB 7 TAAAGLLLLAQAQAMADIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQKSP 66
QY 65 QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFSTPTFTGGGTKL 124
DB 67 QLLVYNKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFSTPTFTGGGTKL 126
QY 125 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWT 184
DB 127 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWT 186
QY 185 DQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPTIVKSFNRNEC 234
DB 187 DQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPTIVKSFNRNEC 236

RESULT 4

AY30122 standard; Protein; 236 AA.
AY30122;
20-OCT-1999 (first entry)
Murine anti-botulinum toxin antibody fragment (BotFab 22) light chain.
Recombinant antibody fragment; rFab; botulinum; neurotoxin;
Clostridium botulinum; detection.
Mus musculus.
US5932449-A.
03-AUG-1999.
30-JAN-1997; 97US-0792824.
01-FEB-1996; 96US-0011013.
30-JAN-1997; 97US-0792824.
(USSA) US SEC OF ARMY.
Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;
WPI; 1999-492692/41.
N-PSDB; AAX86666.
Detection of botulinum toxin
Claim 25; Columns 39-40; 24pp; English.
This sequence represents the light chain of BotFab 22,
a murine recombinant antibody fragment (rFab) specific to
botulinum toxin types A and B. A cDNA library was made from mouse mRNA
isolated from mice immunised with human pentavalent toxoid. The cloned
mouse heavy and light chains were expressed in phage display libraries
and screened for their ability to bind to botulinum toxin types A or B.
The clones were then isolated and sequenced. Botulinum neurotoxin is
produced as several antigenically distinct serotypes (A-G) and is
non-covalently associated with non-neurotoxic proteins. The rFab of
this invention binds to the non-neurotoxic proteins. The rFab of
neurotoxin complexes A and B. Such antibody fragments are able to
act as immunosensors for detecting botulinum toxins in food and
are also useful in health care and in military applications. They
are less expensive to produce than monoclonal antibodies as they can be
isolated from large scale bacterial cultures. Also, the affinity of an
rFab may be altered by mutagenesis of its gene and subsequent screening
of the expressed rFabs.

Query Match 91.7%; Score 1131; DB 20; Length 236;
Best Local Similarity 93.9%; Pred. No. 2.2e-64;
Matches 216; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
QY 5 TQVLALLLWLTGARCIDIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQKSP 64
DB 7 TAAAGLLLLAQAQAMADIQMTQSPASLSASVGETVTITCRASGNITQNYLAWYQQTQKSP 66
QY 65 QLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFSTPTFTGGGTKL 124
DB 67 QLLVYNKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYVCOHFSTPTFTGGGTKL 126
QY 125 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWT 184
DB 127 EIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWT 186
QY 185 DQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPTIVKSFNRNEC 234

Db 187 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 236
 |||

RESULT 5
 ID AAY30118
 AC AAY30118 standard; Protein; 233 AA.

XX AAY30118;

XX 20-OCT-1999 (first entry)

XX Murine anti-botulinum toxin antibody fragment (BotFab 1) light chain.

XX Recombinant antibody fragment; rFab; botulinum; neurotoxin;
 Clostridium botulinum; detection.

XX Mus musculus.

XX US5932449-A.

XX 03-AUG-1999.

XX 30-JAN-1997; 97US-0792824.

XX 01-FEB-1996; 96US-0011013.

XX 30-JAN-1997; 97US-0792824.

XX (USSA) US SEC OF ARMY.

XX Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;

XX WPI; 1999-492692/41.

XX N-PSDB; AAX86665.

XX Detection of botulinum toxin

XX Claim 8; Columns 25-26; 24pp; English.

XX This sequence represents the light chain of BotFab 1,
 a murine recombinant antibody fragment (rFab) specific to
 botulinum toxin types A and B. A cDNA library was made from mouse mRNA
 isolated from mice immunised with human pentavalent toxoid. The cloned
 mouse heavy and light chains were expressed in phage display libraries
 and screened for their ability to bind to botulinum toxin types A or B.
 The clones were then isolated and sequenced. Botulinum neurotoxin is
 produced as several antigenically distinct serotypes (A-G) and is
 non-covalently associated with non-neurotoxic proteins. The rFab of
 this invention binds to the non-neurotoxic proteins that are found in
 neurotoxin complexes A and B. Such antibody fragments are able to
 act as immunosensors for detecting botulinum toxins in food and
 are also useful in health care and in military applications. They
 are less expensive to produce than monoclonal antibodies as they can
 be isolated from large scale bacterial cultures. Also, the affinity of an
 rFab may be altered by mutagenesis of its gene and subsequent screening
 of the expressed rFabs.

XX Sequence 233 AA;

Query Match 87.5%; Score 1080; DB 20; Length 233;

Best Local Similarity 92.0%; Pred. No. 3.7e-61;

Matches 206; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 5 TVLALLLLLTGARCIDIOMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTGKSP 64

XX 7 TAAAGLLLLAQAQPMADIQMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTGKSP 66

XX 65 QLLVYSAKTLADGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWMSTPYTGGTKL 124

XX 67 QLLVYNAKTLADGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWMSTPYTGGTKL 126

XX 125 EIKRADAAPTVSIFFPPSSQTLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVLSWT 184

Db 127 EIKRADAAPTVSIFFPPSSQTLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVLSWT 186
 QY 185 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKS 228
 |||
 Db 187 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKS 230

RESULT 6

AAV14557

XX AAV14557 standard; Protein; 234 AA.

XX AAV14557;

XX 31-AUG-1999 (first entry)

XX Anti-p21(ras) monoclonal antibody Y13-259 light chain.

XX Inhibition; function; recombinant; p21; ras; monoclonal antibody;

XX light chain; activity; cancer; neoplasm; oncogene.

XX Mus sp.

XX US5919650-A.

XX 06-JUL-1999.

XX 22-APR-1991; 91US-0690192.

XX 22-APR-1991; 91US-0690192.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Barbacid M, Montano X;

XX WPI; 1999-394621/33.

XX N-PSDB; AAX79347.

XX Inhibiting protein function using recombinant, intracellularly

XX expressed antibodies

XX Example 1; Column 15-16; 23pp; English.

XX The invention relates to a method for inhibiting protein function using
 recombinant, intracellularly expressed anti-protein antibodies (or
 fragments). The protein function to be inhibited is preferably p21(ras).
 It is especially inhibited by the monoclonal antibody Y13-259. This
 sequence represents the light chain of the Y13-259 antibody. The method
 may be used to inhibit the activity of specific proteins in cells and
 eliminate undesirable biological responses, e.g. it may be used to treat
 conditions associated with the over-expression or overactivity of the
 target protein. In this way the method may be used to treat cancer and
 neoplasms, by targeting proteins encoded by oncogenes.

XX Sequence 234 AA;

Query Match 77.4%; Score 955; DB 20; Length 234;

Best Local Similarity 76.9%; Pred. No. 3e-53;

Matches 180; Conservative 25; Mismatches 29; Indels 0; Gaps 0;

QY 1 MSVLTQVLALLLLLTGARCIDIOMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTQ 60

Db 1 MAIPTQLGLLLLTGARCIDIOMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTQ 60

QY 61 GKSPQLLYYSAKTLADGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWMSTPYTGG 120

Db 61 GKSPQLLYYASSLODGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWMSTPYTGG 120

QY 121 GTKLEIKRADAAPTVSIFFPPSSQTLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVL 180

Db 121 GTKLEIKRADAAPTVSIFFPPSSQTLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVL 180

QY 181 NSWTDQDQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSFNREC 234

Db 181 DSVTDQDSKSTYSMSSTLSLTKVEYERHNLTYTCEVVHKTSSSPVYKSFNRNEC 234

RESULT 7
AAW27089
ID AAW27089 standard; Protein; 214 AA.
XX AC
XX AAW27089;
XX 18-NOV-1997 (first entry)
XX Mouse monoclonal antibody B9 light chain.
XX DE
XX Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;
XX KW antibody; Fab.
XX OS
XX Mus musculus.
XX Key Location/Qualifiers
XX Region 24..34
XX FT /label= CDR1
XX FT 50..56
XX FT /label= CDR2
XX FT 89..97
XX FT /label= CDR3
XX FT 108..214
XX FT /label= Ckappa
XX JP09154587-A.
XX 17-JUN-1997.
XX 09-MAY-1996; 96JP-0114492.
XX 02-NOV-1995; 95KR-0039459.
XX (KOAD) KOREAN SCI & TECHNOLOGY RES CENT.
XX WPI; 1997-367067/34.
XX N-PSDB; AAT85091.
XX DNA encoding mouse antibody binding human plasma apo-lipoprotein
XX B-100 - useful for removing arteriosclerotic lipoprotein(s)
XX Claim 4; Fig 6; 17pp; Japanese.
XX The present sequence represents the mouse monoclonal antibody B9 light
XX chain (B9L), which binds specifically to human blood apolipoprotein
XX B-100. The nucleic acid can be used in a method for the preparation
XX of a reconstituted antibody which specifically binds human plasma
XX apolipoprotein B-100. The antibody can be used as a reagent for
XX determining the concentration of human plasma apolipoprotein B-100
XX in a sample. The antibody is also useful in a drug composition for
XX selectively removing arteriosclerotic lipoproteins containing human
XX plasma apolipoprotein B-100.
XX Sequence 214 AA;
Query Match 76.7%; Score 947; DB 18; Length 214;
Best Local Similarity 83.6%; Pred. No. 8.9e-53;
Matches 179; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 21 DIOMTQSPASLSASVGETVITTCRAGNIQYLAQQTGKSPQLLVYSAKTLADGVPS 80
DB 1 DIKMTQSPSMYASLGERVTITTCRAGNIQYLAQQTGKSPQLLVYSAKTLADGVPS 60
QY 81 RFSGSGSGTQYSLK INSLQPEFGSYCOHFWSTPTTFGGGKLEIKRADAAPTVSIFPP 140
DB 61 RFSGSGSGQDYSLTISLSEYEDLGIYICLQDFEPTTFGGGKLEIKRADAAPTVSIFPP 120
QY 141 SSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSNSTDQDSKSTYSMSSTLT 200
DB 121 SSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLSNSTDQDSKSTYSMSSTLT 180

QY 201 LTKDEYERHNSYTCEATHKTTSTPIVKSFNRENC 234
DB 181 LTKDEYERHNSYTCEATHKTTSTPIVKSFNRENC 214

RESULT 8
AAR76087
ID AAR76087 standard; Protein; 239 AA.
XX AC
XX AAR76087;
XX 21-NOV-1995 (first entry)
XX MAB 55.1 light chain.
XX Antigen binding structure; complementarity determining region; CDR;
XX CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
XX monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
XX transgenic animal; transgenic plant; antibody engineering;
XX humanized antibody; immunotoxin.
XX Mus sp.
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= sig_peptide
XX FT 21..239
XX FT /label= Mat_protein
XX FT /note= "claim 3, page 98"
XX WO9515382-A.
XX 08-JUN-1995.
XX 29-NOV-1994; 94WO-GB02610.
XX 03-JUN-1994; 94GB-0011089.
XX 03-DEC-1993; 93GB-0024819.
XX (ZENE) ZENECA LTD.
XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
XX Rose MS, Wright AF;
XX WPI; 1995-215262/28.
XX N-PSDB; AAQ94036.
XX Antigen binding structures containing CDRs recognising the CA55.1
XX antigen - produced by hybridomas and host cells, for use in the
XX diagnosis and therapy of cancer
XX Disclosure; Fig.16; 121pp; English.
XX MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
XX antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)
XX chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
XX V-min humanized 55.1 constructs have been expressed in myeloma
XX cells and E. coli.
XX Sequence 239 AA;
Query Match 75.4%; Score 930.5; DB 16; Length 239;
Best Local Similarity 75.0%; Pred. No. 1.1e-51;
Matches 180; Conservative 22; Mismatches 31; Indels 7; Gaps 2;

QY 1 MSVLTVQVLAALLLWLTGARCIDIOMTQSPASLSASVGETVITTCRAGNI-----QNYLA 54
DB 1 MDQAQVLIILLWVSGTCGDIYMSQSPSLAVSAGEKVTMSCKSSQSLNLSRTRKNYLA 60
QY 55 WYQQTQCKSPQLLVYSAKTLADGVPSRFGSGSGTQYSLKINSIQPEDFGSYCOHFWST 114
DB 61 WYQQRPGQPKLLIYWASTRTSGVPDFTGSGSGTDFTLTISVQAEDLAIYYCKQSY-T 119

1 MSLVTOVLALLLWLTGACDIOMTQSPASLSASVGETVTITCRASGNI-----QNYLAWY 56
1 METDTILLWLLWVPGSTGDIVLTQSPASLAVSLGORATISCKASQSDYDGDYSYNNWY 60
57 QOTGKSPQLLVYSAKTLADGVPFRSGSGSGTQYSLKINSLOPEDFGSYCQHFSTPY 116
61 QOKPGQPKLLIYAASNULESGIPARFSGSGSGTDTLNIHPVEEEDAATYYCQOOTNEDPW 120
117 TFGGTTKLEIKRADAPTIVSIFPPSSQQLTSGGASVVCFLNFPKDNVKKWIDGSRQ 176
121 TFGGTTKLEIKRADAPTIVSIFPPSSQQLTSGGASVVCFLNFPKDNVKKWIDGSRQ 180
177 NGVLNSWTDQSDKSTYSMSSTLTLTDEYERHNSYTCEATHKSTSPIVKSFNRNEC 234
181 NGVLNSWTDQSDKSTYSMSSTLTLTDEYERHNSYTCEATHKSTSPIVKSFNRNEC 238

RESULT 10
AAW15935
ID AAW15935 standard; Protein; 216 AA.
XX
AC AAW15935;
DT 09-DEC-1997 (first entry)
XX
DE Antibody 3G2 light chain variable region.
XX
KW catalytic antibody; enantioselective hydrolysis; hybridoma;
KW ZAA7G12; ZAA3G2; ds.
XX
OS Mus.
FH Key Location/Qualifiers
FT Misc-difference 215 /note= "encoded by TAA"
XX
XX WO9629426-A1.
XX
XX 26-SEP-1996.
XX
XX 17-MAR-1995; 95WO-JP00462.
XX
XX 17-MAR-1995; 95WO-JP00462.
XX
XX (PROT-) PROTEIN ENG RES INST.
XX
XX Fujii I, Kinoshita K, Tanaka F;
XX
XX WPI: 1996-443199/44.
XX
XX N-PSDB; AAT87818.
XX
XX Catalytic antibody for enantioselective hydrolysis of amino acid
XX esters - also new hybridoma secreting the antibody
XX
XX Disclosure; Page 39; 49pp; Japanese.
XX
XX The patent discloses new catalytic antibodies which hydrolyse amino
XX acid esters enantioselectively. Preferably the esters are 4-nitro-
XX benzyl esters and the esterified amino acids are amino-protected.
XX Also disclosed are new hybridomas expressing the catalytic antibodies,
XX especially ZAA7G12 (FERM BP-4947) and ZAA3G2 (FERM BP-4946). The
XX antibodies are raised in mice using the compound p-nitrobenzyl
XX [4-carboxy-1-(benzyloxy-carbonyl-amino)-butyl]phosphonate as hapten.
XX They are used for efficient resolution of racemic amino acids with
XX high optical selectivity, giving optically active amino acids useful
XX for the production of optically active drugs and chiral separation
XX agents.
XX The present sequence represents the variable region of the light chain
XX of antibody 3G2, produced by the hybridoma ZAA3G2.
XX
XX Sequence 216 AA;
SQ Query Match 74.9%; Score 924; DB 17; Length 216;

115 PYTFGGTGLEIKRADAPTIVSIFPPSSQQLTSGGASVVCFLNFPKDNVKKWIDGSE 174
120 LRTFGGTTKLEIKRADAPTIVSIFPPSSQQLTSGGASVVCFLNFPKDNVKKWIDGSE 179
175 RONGVLNSWTDQSDKSTYSMSSTLTLTDEYERHNSYTCEATHKSTSPIVKSFNRNEC 234
180 RONGVLNSWTDQSDKSTYSMSSTLTLTDEYERHNSYTCEATHKSTSPIVKSFNRNEC 239

RESULT 9
AAE18371
D AAE18371 standard; Protein; 238 AA.
E AAE18371;
T
X
X 07-MAY-2002 (first entry)
X Human penton base monoclonal antibody, DAV-1 light chain.
X Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
X vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
X hyperproliferative disorder; hormonal disorder; DAV-1 light chain;
X cytostatic; vasotropic; ophthalmological.
X Homo sapiens.
X
X WO200204522-A2.
X
X 17-JAN-2002.
X
X 09-JUL-2001; 2001WO-EP07878.
X
X 10-JUL-2000; 2000US-0613017.
X
X (NOVS) NOVARTIS AG.
X (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
X (SCRI) SCRIPPS RES INST.
X
X Nemerow GR, Li E;
X
X WPI: 2002-171707/22.
X
X N-PSDB; RAD29309.
X
X New bifunctional molecules comprising an antibody or its
X antigen-binding portion, and a targeting agent, useful for e.g. gene
X therapy, or for promoting Adenoviral vector-mediated gene delivery to
X cells lacking av integrins
X
X Claim 11; Page 93; 106pp; English.
X
X The present invention relates to a bifunctional molecule comprising an
X antibody or its antigen-binding portion, and a targeting agent where the
X antibody specifically binds to an antigen in a protein that binds to av
X integrin, and the targeting agent specifically binds to a cell surface
X protein that activates the phosphatidylinositol 3 (PI3K) signalling
X pathway. The bifunctional molecules are useful for gene therapy, for
X promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
X av integrins, for enhancing Ad binding and internalisation, and in gene
X delivery of by fibreless adenovirus particles. The bifunctional molecules
X permit targeting of viral and bacterial vectors to cells that express
X targeted receptors. Diseases that can be targeted include cancers,
X vascular disorders, diabetic retinopathies, restenosis, ophthalmic
X disorders, hyperproliferative disorders, and hormonal disorders.
X The present sequence is human penton base monoclonal antibody, DAV-1
X light chain.
X
X Sequence 238 AA;
SQ Query Match 75.0%; Score 925; DB 23; Length 238;
Best Local Similarity 73.1%; Pred. No. 2.4e-51;
Matches 174; Conservative 27; Mismatches 33; Indels 4; Gaps 1;

Best Local Similarity 81.3%; Pred. No. 2.6e-51;
Matches 174; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 21 DIQMTQSPASLSASVGETVTITCRASGNITQYQVQOTGKSPQLLVYSAKTLADGVPS 80
Db 1 ELVMTQSPASLSASVGETVTITCRASGNITQYQVQOTGKSPQLLVYSAKTLADGVPS 60

QY 81 RFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGKLEIKRADAAAPTYSIFPP 140
Db 61 RFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPYTFGGGKLEIKRADAAAPTYSIFPP 120

QY 141 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQSDKSDSYMSSTLT 200
Db 121 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQSDKSDSYMSSTLT 180

QY 201 LTKDEYERHNSYTCETHKTSPIVKSFNNEC 234
Db 181 LTKDEYERHNSYTCETHKTSPIVKSFNNEC 214

RESULT 11
AAW83042
ID AAW83042 standard; Protein; 238 AA.
AC AAW83042;
XX
XX 15-MAR-1999 (first entry)
XX Anti-Fas Mab HFE7A light chain.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apotosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocardiitis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy; complementarity determining region;
KW CDR.

XX
OS Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein /label= Sig_peptide
XX 21..238
XX Region /label= Mat_protein
XX 21..131
XX Region /label= variable
XX 132..238
XX Region /label= Constant
XX 44..58
XX Region /label= CDR_L1
XX /note= "claim 9"
XX 74..80
XX Region /label= CDR_L2
XX /note= "claim 9"
XX 113..121
XX Region /label= CDR_L3
XX /note= "claim 9"
XX
XX A09859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.

(SANY) SANKYO CO LTD.
Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
WPI: 1998-543440/47.
N-PSDB; AAV70130.
New antibodies and proteins bind conserved epitope of Fas antigen -
used to evaluate drugs in animal models and to treat Fas-associated
diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
myocarditis, hepatitis and AIDS
Reference Example 4; Page 189-190; 292pp; English.
This is the amino acid of the light chain of murine anti-human Fas
monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light
chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
RNA by RT-PCR (see AAV70127-28). The invention provides humanised
HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
antibodies are capable of inducing apoptosis in abnormal cells
expressing Fas, and of inhibiting Fas-induced apoptosis in normal
cells. They are used to evaluate, in animal models, treatments of
diseases that involve Fas/Fas ligand interactions, and also to treat
such diseases, including autoimmune disease (e.g. systemic lupus
erythematosus, Hashimoto's disease, graft versus host disease,
scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
anaemia, hepatitis, AIDS and transplant rejection (all claimed).

XX Sequence 238 AA;
SQ

Query Match 74.4%; Score 918; DB 19; Length 238;
Best Local Similarity 72.3%; Pred. No. 6.7e-51;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;

QY 1 MSVLTVALLLLLTGARDIOMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
Db 1 METDTILLWVLMWIPGSTGDIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMYWY 60

QY 57 QQTQKSPOLLVYSAKTLADGVPSRFGSGSGTQYSLKINSLOPEDFGSYCOHFWSTPY 116
Db 61 QOKPGOPPKLLIYAASNLSEGIAPRFGSGSGTDFTLNHPVEEDATYTCQSDNEDPR 120

QY 117 TFGGGTKLEIKRADAAAPTYSIFPPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQ 176
Db 121 TFGGGTKLEIKRADAAAPTYSIFPPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQ 180

QY 177 NGVLNSWTDQSDKSDSYMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 234
Db 181 NGVLNSWTDQSDKSDSYMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNEC 238

RESULT 12
AAW83042
ID AAW83042 standard; Protein; 238 AA.
XX AAW83042;
XX
XX 24-NOV-2000 (first entry)
XX
XX Mouse anti-Fas antibody HFE7A light chain.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

KW hepatitis; AIDS; graft rejection; light chain.
 XX Mus musculus.
 XX JP2000169393-A.
 XX 20-JUN-2000.
 PD 30-SEP-1999; 99JP-0278301.
 PF 30-SEP-1998; 98JP-0276883.
 PR (SANY) SANKYO CO LTD.
 XX WPI; 2000-485645/43.
 XX N-PSDB; AAA72109.
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody .
 XX Example 4; Page 70; 139pp; Japanese.
 PS The invention relates to compositions for the prevention or treatment
 XX or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanized version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. The present sequence represents the
 CC light chain of the murine anti-human Fas monoclonal antibody HFE7A,
 CC which is produced by hybridoma HFE7A (FERM-BP-5828).
 XX Sequence 238 AA;
 SQ Query Match 74.4%; Score 918; DB 21; Length 238;
 Best Local Similarity 72.3%; Pred. No. 6.7e-51;
 Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;
 QY 1 MSVLTQVLAALLLWLTGARCQDQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
 DB 1 METDTILLVWMLWLPSTGDIIVLTQSPASLAVSLGQRATISCKASQSDYDGDGYMNNY 60
 QY 57 QOTQCKSPOLLVYSAKTLADGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWSPTY 116
 DB 61 QOKPGPKLLIYAASNLSEGIPIARFSGSGGTDFTLNHPVEEDAATYICQSQNEDPR 120
 QY 117 FPGGKLEIKRADAAPTVSPFPPSEQLTSGASVCFNLNFKDINVKWKIDGSRQ 176
 DB 121 FPGGKLEIKRADAAPTVSPFPPSEQLTSGASVCFNLNFKDINVKWKIDGSRQ 180
 QY 177 NGVLNSWTDQDQSDKSTYSMSPTLTLDKDEYRHNSYTCATHKTSTPTVKSFNRNEC 234
 DB 181 NGVLNSWTDQDQSDKSTYSMSPTLTLDKDEYRHNSYTCATHKTSTPTVKSFNRNEC 238
 RESULT 13
 AAW90898
 ID AAW90898 standard; Protein; 238 AA.
 AC AAW90898;
 XX 08-AUG-2000 (first entry)
 XX Murine anti-Fas antibody HFE7A light chain protein.
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Mus musculus.
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tanaki I, Takahashi T;
 PI WPI; 2000-258930/23.
 XX N-PSDB; AAA11547.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems .
 XX Example reference 4; Page 104; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the
 CC method of the invention.
 XX Sequence 238 AA;
 SQ Query Match 74.4%; Score 918; DB 21; Length 238;
 Best Local Similarity 72.3%; Pred. No. 6.7e-51;
 Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1;
 QY 1 MSVLTQVLAALLLWLTGARCQDQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
 DB 1 METDTILLVWMLWLPSTGDIIVLTQSPASLAVSLGQRATISCKASQSDYDGDGYMNNY 60
 QY 57 QOTQCKSPOLLVYSAKTLADGVPSRFGSGSGCTQYSLKINSLOPEDFGSYCOHFWSPTY 116

121	TFGGTKLEIKRDAAPTYSIFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSEQ	180
Db		
177	NGVLNSWTDQDSKSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	234
QY		
181	NGVLNSWTDQDSKSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC	238
Db		
RESULT 15		
ABB74913		
ID	ABB74913	standard: Peptide: 238 AA.

RESULT 15	
ABB74913	
ID	ABB74913 standard; Peptide: 238 AA.
XX	
XX	
AC	ABB74913;
XX	
XX	
DT	30-APR-2002 (first entry)
XX	
XX	
DE	Humanised anti-Fas antibody related peptide SEQ ID NO 3.
XX	
XX	
KW	Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;
KW	heavy chain; apoptosis; anti-allergic; immunosuppressive; apoptotic;

[illegible]

XX
XX
PT
PT
XX
XX
PS
PS
XX

Drugs for preventing or treating e.g. autoimmune disease or allergy,
comprises humanised anti-Fas antibody -
Disclosure; Page 65; 154pp; Japanese.

The invention relates to a preventive or treating agent for diseases
caused by abnormality in the Fas/Fas ligand system containing, as the
active component, an antibody having a light chain subunit and a heavy
chain subunit and an activity of combining specifically with mammalian

CC ras and an activity of inducing apoptosis in a cell expressing ras. The
CC agent has antiallergic, immunosuppressive and apoptotic activity and is
CC used for preventing and treating autoimmune diseases, allergy, atopy and
CC others. The present sequence is that of a peptide useful to the
CC invention.

XX
SQ Sequence 238 AA;

Query Match 74.4%; Score 918; DB 23; Length 238;
Best Local Similarity 72.3%; Pred. No. 6.7e-51;
Matches 172; Conservative 28; Mismatches 34; Indels 4; Gaps 1

[illegible]

QY	117	TFGGTKEIKRAADAPTVISIFPPSSBQLTSGGASVVCFLNNFYPKIDINVKKIDGSRQ	176
Db	121	TFGGTKEIKRAADAPTVISIFPPSSBQLTSGGASVVCFLNNFYPKIDINVKKIDGSRQ	180
QY	177	NGVLNSWTDQSKDSTYSMSSTLTLTKDYEYRINSYTCEATHKTSIPVKSFNRNEC	234
Db	181	NGVLNSWTDQSKDSTYSMSSTLTLTKDYEYRINSYTCEATHKTSIPVKSFNRNEC	238

Tue Jul 1 18:41:05 2003

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Search completed: June 18, 2003, 16:44:19
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